

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2004, 14:10:29 ; Search time 23 Seconds
(without alignments)
-733.987 Million cell updates/sec

Title: US-09-787-844-2

Perfect score: 1792

Sequence: 1 KRQRQAGAEANGARGAL.....PSWPLLPFLNLALPLGPV 327

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA: *
1: /cgn2_6/prodata/2/iaa/5A-COMB.pep: *
2: /cgn2_6/prodata/2/iaa/5B-COMB.pep: *
3: /cgn2_6/prodata/2/iaa/5A-COMB.pep: *
4: /cgn2_6/prodata/2/iaa/5B-COMB.pep: *
5: /cgn2_6/prodata/2/iaa/5A-COMB.pep: *
6: /cgn2_6/prodata/2/iaa/5B-COMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1728	96.4	314	3	US-09-008-271A-3
2	1728	96.4	314	4	US-09-907-794A-257
3	1728	96.4	314	4	US-09-905-125A-257
4	1728	96.4	314	4	US-09-902-775A-257
5	1723	96.1	314	4	US-09-023-942A-6
6	1701	94.9	312	4	US-09-023-942A-4
7	1419	79.2	306	4	US-09-386-642-53
8	1108.5	61.9	285	4	US-09-023-942A-26
9	574	32.0	290	4	US-09-386-653A-7
10	554	30.9	299	3	US-08-944-483-66
11	550	30.7	315	4	US-09-386-653A-9
12	541.5	30.2	328	4	US-09-386-642-11
13	540.5	30.2	319	4	US-09-386-642-12
14	531.5	29.7	317	4	US-09-386-629-7
15	531.5	29.7	317	4	US-09-907-794A-263
16	531.5	29.7	317	4	US-09-905-125A-263
17	531.5	29.7	317	4	US-09-902-775A-263
18	528.5	29.5	270	2	US-08-978-404B-8
19	515	28.7	273	2	US-09-016-366A-19
20	515	28.7	273	2	US-08-978-404B-14
21	514	28.7	274	2	US-09-016-366A-21
22	514	28.7	274	2	US-08-978-404B-15
23	512	28.6	267	2	US-09-016-366A-23
24	512	28.6	267	2	US-08-978-404B-18
25	512	28.6	276	2	US-09-016-366A-15
26	512	28.6	276	2	US-08-978-404B-21
27	511	28.5	638	2	US-08-681-151-3

28	509.5	28.4	273	2	US-08-978-404B-6	Sequence 6, Appli
29	507	28.3	273	2	US-08-978-404B-3	Sequence 3, Appli
30	507	28.3	454	3	US-09-518-046-2	Sequence 2, Appli
31	506	28.2	327	4	US-09-386-629-8	Sequence 8, Appli
32	505	28.2	248	3	US-08-944-483-63	Sequence 63, Appli
33	504	28.1	275	2	US-09-016-366A-17	Sequence 17, Appli
34	504	28.1	275	2	US-08-978-404B-12	Sequence 12, Appli
35	503.5	28.1	249	3	US-09-079-970A-5	Sequence 5, Appli
36	500	27.9	274	2	US-08-978-404B-5	Sequence 4, Appli
37	497.5	27.8	244	4	US-09-601-318-4	Sequence 5, Appli
38	497.5	27.8	244	4	US-09-601-318-5	Sequence 6, Appli
39	497.5	27.8	244	4	US-09-601-318-6	Sequence 7, Appli
40	497.5	27.8	244	4	US-09-601-318-7	Sequence 7, Appli
41	497.5	27.8	245	3	US-09-079-970A-6	Sequence 6, Appli
42	497.5	27.7	284	4	US-09-601-318-1	Sequence 1, Appli
43	496.5	27.7	284	4	US-09-387-375-7	Sequence 7, Appli
44	493.5	27.5	245	3	US-08-944-483-69	Sequence 69, Appli
45	489.5	27.3	418	1	US-08-508-448C-25	Sequence 25, Appli

ALIGNMENTS

RESULT 1

US-09-008-271A-3
; Sequence 3, Application US/09008271A
; Patent No. 6203979
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Hillman, Jennifer L.
; Yue, Henry
; Guegler, Karl J.
; Corley, Neil C.
; Tang, Tom Y.
; Shah, Purvi
; TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/008,271A
; FILING DATE: 16-Jan-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mohan-Peterson, Sheela
; REGISTRATION NUMBER: 41,201
; REFERENCE/DOCKET NUMBER: PF-0458 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PROSTUT03
; CLONE: 789927
; SEQUENCE DESCRIPTION: SEQ ID NO: 3 :

US-09-008-271A-3

Query Match 96.4%; Score 1728; DB 3; Length 314;
Best Local Similarity 100.0%; Pred. No. 6.9e-166;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 MGARGALLALLARAGLRKPESQEAAPLSGPGRRVITSRIVGGEDAEGLRWPMQGSLLR 73
DB 1 MGARGALLALLARAGLRKPESQEAAPLSGPGRRVITSRIVGGEDAEGLRWPMQGSLLR 60

QY 74 LWDSHVCGVSLLSHRWALTAHCFETYSDLSDPGMMVQFGQLTSPSPFWSLQAYYTRYF 133
DB 61 LWDSHVCGVSLLSHRWALTAHCFETYSDLSDPGMMVQFGQLTSPSPFWSLQAYYTRYF 120

QY 134 VSNIIYSPRYLGNSPYDIALVKLSAPVYTKHIQPICLQASTFEFENRTDCWVTGMYIK 193
DB 121 VSNIIYSPRYLGNSPYDIALVKLSAPVYTKHIQPICLQASTFEFENRTDCWVTGMYIK 180

QY 194 EDEALPSFHTLQEVQVAIINNSMNCNHLFLKYSFRKDIFGDMVCAGNAQGGKACFGDSGG 253
DB 181 EDEALPSFHTLQEVQVAIINNSMNCNHLFLKYSFRKDIFGDMVCAGNAQGGKACFGDSGG 240

QY 254 PLACNKNGLMYQIGVSWGVCGRRPNRPVYTNISHHFEWIKLMAQSGMSQDPSPWPLL 313
DB 241 PLACNKNGLMYQIGVSWGVCGRRPNRPVYTNISHHFEWIKLMAQSGMSQDPSPWPLL 300

QY 314 FFPLLWALPLLGPV 327
DB 301 FFPLLWALPLLGPV 314

RESULT 2

US-09-907-794A-257
Sequence 257, Application US/09907794A

Patent No. 6635468

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillar, Kenneth, J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28

PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 257
LENGTH: 314
TYPE: PRT
ORGANISM: Homo Sapien
US-09-907-794A-257

Query Match

Best Local Similarity 100.0%; Pred. No. 6.9e-166; Length 314;

Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 MGARGALLALLARAGLRKPESQEAAPLSGPGRRVITSRIVGGEDAEGLRWPMQGSLLR 73
DB 1 MGARGALLALLARAGLRKPESQEAAPLSGPGRRVITSRIVGGEDAEGLRWPMQGSLLR 60

QY 74 LWDSHVCGVSLLSHRWALTAHCFETYSDLSDPGMMVQFGQLTSPSPFWSLQAYYTRYF 133
DB 61 LWDSHVCGVSLLSHRWALTAHCFETYSDLSDPGMMVQFGQLTSPSPFWSLQAYYTRYF 120

QY 134 VSNIIYSPRYLGNSPYDIALVKLSAPVYTKHIQPICLQASTFEFENRTDCWVTGMYIK 193
DB 121 VSNIIYSPRYLGNSPYDIALVKLSAPVYTKHIQPICLQASTFEFENRTDCWVTGMYIK 180

QY 194 EDEALPSFHTLQEVQVAIINNSMNCNHLFLKYSFRKDIFGDMVCAGNAQGGKACFGDSGG 253
DB 181 EDEALPSFHTLQEVQVAIINNSMNCNHLFLKYSFRKDIFGDMVCAGNAQGGKACFGDSGG 240

QY 254 PLACNKNGLMYQIGVSWGVCGRRPNRPVYTNISHHFEWIKLMAQSGMSQDPSPWPLL 313
DB 241 PLACNKNGLMYQIGVSWGVCGRRPNRPVYTNISHHFEWIKLMAQSGMSQDPSPWPLL 300

QY 314 FFPLLWALPLLGPV 327
DB 301 FFPLLWALPLLGPV 314

RESULT 3

US-09-905-125A-257
Sequence 257, Application US/09905125A

Patent No. 6664376

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone

; PRIOR FILING DATE: 1999-10-05
 ; PRIOR APPLICATION NUMBER: PCT/US99/28214
 ; PRIOR FILING DATE: 1999-11-29
 ; PRIOR APPLICATION NUMBER: PCT/US99/28313
 ; PRIOR FILING DATE: 1999-11-30
 ; PRIOR APPLICATION NUMBER: PCT/US99/28564
 ; PRIOR FILING DATE: 1999-12-02
 ; PRIOR APPLICATION NUMBER: PCT/US99/28565
 ; PRIOR FILING DATE: 1999-12-02
 ; PRIOR APPLICATION NUMBER: PCT/US99/30095
 ; PRIOR FILING DATE: 1999-12-16
 ; PRIOR APPLICATION NUMBER: PCT/US99/30911
 ; PRIOR FILING DATE: 1999-12-20
 ; PRIOR APPLICATION NUMBER: PCT/US99/30999
 ; PRIOR FILING DATE: 1999-12-20
 ; PRIOR APPLICATION NUMBER: PCT/US00/00219
 ; PRIOR FILING DATE: 2000-01-05
 ; NUMBER OF SEQ ID NOS: 423
 ; SEQ ID NO 257
 ; LENGTH: 314
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-09-902-775A-257

Query Match 96.4%; Score 1728; DB 4; Length 314;
 Best Local Similarity 100.0%; Pred. No. 6.9e-166;
 Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	14	MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAEGLGRWPQGSRLR	73
Db	1	MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAEGLGRWPQGSRLR	60
QY	74	LWDHSVGVSLLSHRWALTAHCFETYSDLSDPGMMVQFGLTSPFWSLQAYTRYF	133
Db	61	LWDHSVGVSLLSHRWALTAHCFETYSDLSDPGMMVQFGLTSPFWSLQAYTRYF	120
QY	134	VSNYILSPRYLGNSPYDIALVKLSAPVYTKHIQPICLQASTFEFENRTDCWVTGWGYIK	193
Db	121	VSNYILSPRYLGNSPYDIALVKLSAPVYTKHIQPICLQASTFEFENRTDCWVTGWGYIK	180
QY	194	EDEALPSPHTLQEVQVVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKACFGDSGG	253
Db	181	EDEALPSPHTLQEVQVVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKACFGDSGG	240
QY	254	PLACNKNGLWYQIGVSWGVCGRPNRPVYTNISHHFEWIKLMAQSGMSQDPSPWPLL	313
Db	241	PLACNKNGLWYQIGVSWGVCGRPNRPVYTNISHHFEWIKLMAQSGMSQDPSPWPLL	300
QY	314	FFPLLWALPLLGPV	327
Db	301	FFPLLWALPLLGPV	314

RESULT 5
 US-09-023-942A-6
 ; Sequence 6, Application US/09023942A
 ; Patent No. 6479274
 ; GENERAL INFORMATION:
 ; APPLICANT: (US only) ANTALIS Toni Marie and HOOPER John David
 ; TITLE OF INVENTION: NOVEL MOLECULES
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
 ; STREET: 400 GARDEN CITY PLAZA
 ; CITY: GARDEN CITY
 ; STATE: NEW YORK
 ; COUNTRY: USA
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/023,942A
 ; FILING DATE: 13-FEB-1998
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: P05101/97
 ; FILING DATE: 13-FEB-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: P04422/97
 ; FILING DATE: 18-NOV-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: International PCT Application
 ; FILING DATE: 13-FEB-1998
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: DIGIGLIO, FRANK S
 ; REGISTRATION NUMBER: 31,346
 ; REFERENCE/DOCKET NUMBER: 11168
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (516) 742 4343
 ; TELEFAX: (516) 742 4366
 ; TELEX: 230 901 SANS UR
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 314 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-09-023-942A-6

Query Match 96.1%; Score 1723; DB 4; Length 314;
 Best Local Similarity 99.7%; Pred. No. 2.2e-165;
 Matches 313; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	14	MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAEGLGRWPQGSRLR	73
Db	1	MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAEGLGRWPQGSRLR	60
QY	74	LWDHSVGVSLLSHRWALTAHCFETYSDLSDPGMMVQFGLTSPFWSLQAYTRYF	133
Db	61	LWDHSVGVSLLSHRWALTAHCFETYSDLSDPGMMVQFGLTSPFWSLQAYTRYF	120
QY	134	VSNYILSPRYLGNSPYDIALVKLSAPVYTKHIQPICLQASTFEFENRTDCWVTGWGYIK	193
Db	121	VSNYILSPRYLGNSPYDIALVKLSAPVYTKHIQPICLQASTFEFENRTDCWVTGWGYIK	180
QY	194	EDEALPSPHTLQEVQVVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKACFGDSGG	253
Db	181	EDEALPSPHTLQEVQVVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKACFGDSGG	240
QY	254	PLACNKNGLWYQIGVSWGVCGRPNRPVYTNISHHFEWIKLMAQSGMSQDPSPWPLL	313
Db	241	PLACNKNGLWYQIGVSWGVCGRPNRPVYTNISHHFEWIKLMAQSGMSQDPSPWPLL	300
QY	314	FFPLLWALPLLGPV	327
Db	301	FFPLLWALPLLGPV	314

RESULT 6
 US-09-023-942A-4
 ; Sequence 4, Application US/09023942A
 ; Patent No. 6479274
 ; GENERAL INFORMATION:
 ; APPLICANT: (US only) ANTALIS Toni Marie and HOOPER John David
 ; TITLE OF INVENTION: NOVEL MOLECULES
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
 ; STREET: 400 GARDEN CITY PLAZA
 ; CITY: GARDEN CITY
 ; STATE: NEW YORK
 ; COUNTRY: USA
 ; ZIP: 11530

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,942A
FILING DATE: 13-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P05101/97
FILING DATE: 13-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P04022/97
FILING DATE: 18-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: International PCT Application
FILING DATE: 13-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGLIO, FRANK S
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 11168
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742 4343
TELEFAX: (516) 742 4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 312 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-023-942A-4

Query Match 94.9%; Score 1701; DB 4; Length 312;
Best Local Similarity 99.0%; Pred. No. 3.6e-163;
Matches 311; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 14 MGARGALLALLIARAGLRKPESQAAPLSGCGRRVITSRIVGGEDAEELGRWPQGSRLR 73
DB 1 MGARGALLALLIARAGLRKPESQAAPLSGCGRRVITSRIVGGEDAEELGRWPQGSRLR 60
QY 74 LWDSHVCGVSLLSHRWALTAACHCFETYSDLSPSGMWVQFGOLTSMPFSWLSQAYTRYF 133
DB 61 LWDSHVCGVSLLSHRWALTAACHCFET--DLSDPSGMWVQFGOLTSMPFSWLSQAYTRYF 118
QY 134 VSNVILSPRYLGNSPYDIALVKLSAPVYTKHIQICLOASTFEFENRTDCWVTGWGIK 193
DB 119 VSNVILSPRYLGNSPYDIALVKLSAPVYTKHIQICLOASTFEFENRTDCWVTGWGIK 178
QY 194 EDEALPSPHTLQEVQVAIINNSMCHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGG 253
DB 179 EDEALPSPHTLQEVQVAIINNSMCHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGG 238
QY 254 PLACNKNGLWYQIGVVGWVGCGRRNRPVYTNISHHFEWIKLMAQSGMSQPPSWPLL 313
DB 239 PLACNKGDLWYQIGVVGWVGCGRRNRPVYTNISHHFEWIKLMAQSGMSQPPSWPLL 298
QY 314 FPELLWALPLIGPV 327
DB 299 FPELLWALPLIGPV 312

RESULT 7
US-09-386-642-53
Sequence 53, Application US/09386642
Patent No. 6420157
GENERAL INFORMATION:
APPLICANT: Darrow, Andrew
APPLICANT: Qi, Jenson
APPLICANT: Andrade-Gordon, Patricia
TITLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ORT-1028

CURRENT APPLICATION NUMBER: US/09/386,642
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 53
LENGTH: 306
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Fusion gene of
OTHER INFORMATION: human protease P in CFEK2 zymogen vector
US-09-386-642-53

Query Match 79.2%; Score 1419; DB 4; Length 306;
Best Local Similarity 89.7%; Pred. No. 9e-135;
Matches 261; Conservative 4; Mismatches 20; Indels 6; Gaps 2;
QY 23 ALLIARAGLRKP---ESQEAAPLSGCGRRVITSRIVGGEDAEELGRWPQGSRLRWDHSV 79
DB 11 ALLGTTFGCGVPDYKDDDAALAAAFDD---DDKIVGGYVALELGRWPQGSRLRWDHSV 67
QY 80 CGVSLLSHRWALTAACHCFETYSDLSPSGMWVQFGOLTSMPFSWLSQAYTRYFVSNYIL 139
DB 68 CGVSLLSHRWALTAACHCFETYSDLSPSGMWVQFGOLTSMPFSWLSQAYTRYFVSNYIL 127
QY 140 SPYLGNSPYDIALVKLSAPVYTKHIQICLOASTFEFENRTDCWVTGWGIKEDALP 199
DB 128 SPYLGNSPYDIALVKLSAPVYTKHIQICLOASTFEFENRTDCWVTGWGIKEDALP 187
QY 200 SPHTLQEVQVAIINNSMCHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNK 259
DB 188 SPHTLQEVQVAIINNSMCHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNK 247
QY 260 NGLWYQIGVVGWVGCGRRNRPVYTNISHHFEWIKLMAQSGMSQPPDSW 310
DB 248 NGLWYQIGVVGWVGCGRRNRPVYTNISHHFEWIKLMAQSGMSQPPDSW 298

RESULT 8
US-09-023-942A-26
Sequence 26, Application US/09023942A
Patent No. 6479274
GENERAL INFORMATION:
APPLICANT: (US only) ANTALIS Toni Marie and HOOPER John David
TITLE OF INVENTION: NOVEL MOLECULES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: USA
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,942A
FILING DATE: 13-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P05101/97
FILING DATE: 13-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P04022/97
FILING DATE: 18-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: International PCT Application
FILING DATE: 13-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGLIO, FRANK S

```

; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 11168
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742 4343
; TELEFAX: (516) 742 4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 285 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-023-942A-26

Query Match 61.9%; Score 1108.5; DB 4; Length 285;
Best Local Similarity 68.8%; Pred. No. 1.1e-103;
Matches 196; Conservative 36; Mismatches 50; Indels 3; Gaps 2;

QY 42 LSGPCGRRVITSRIVGGDAELGRPMWQSGRLRLWDHSHVCGVSLLSHRWALTAACFCFETYS 101
DB 3 LSGPCGHRITPSRIVGGDAELGRPMWQSLRVGNHLCATLLNRWVLTAACFCQ--K 60

QY 102 DLSDFSGMWVQGGITSMPSFWSLQAYTRFVSNIVLSRYLNSPYDIALVKLSAPVT 161
DB 61 D-NDFPDMTVQSGELTSRPSLWNLQAYSNRYQIEDIFLSPKYSQYENDIALKLSPTV 119

QY 162 YTKHQIPICLOASTFEFNRRIDCWVTGMYIKDEBALPSPHTLQEVQVAIINSMCNHLF 221
DB 120 YNNFQIPICLLNSTYKFENRIDCWVTGWAIGEDESLSPNTLQEVQVAIINSMCNHMY 179

QY 222 LKYSFRKIDFGDMVCAAGNAQGGKACFDGSDGGPLACNKNGLWYQIGVSVGCGGPNRP 281
DB 180 KKPDEFNTNMGVMVCACTPEGGKACFDGSDGGPLACQDVTYVQVGVSVGIGCGPNRP 239

QY 282 GVTNISHHFEVIQKLMQSGMSQDPSPWLLFFPLLWALPLLGP 326
DB 240 GVTNISHYNIQSTMIENGLLRDPVPLLFTLWASSLLRP 284

RESULT 9
US-09-386-653A-7
; Sequence 7, Application US/09386653A
; Patent No. 6458564
; GENERAL INFORMATION:
; APPLICANT: Andrade-Gordon, Patricia
; APPLICANT: Barrow, Andrew
; APPLICANT: Qi, Jian-shen
; TITLE OF INVENTION: DNA encoding the novel human serine
; FILE REFERENCE: ORT-1032
; CURRENT APPLICATION NUMBER: US/09/386,653A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 7
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-386-653A-7

Query Match 32.0%; Score 574; DB 4; Length 290;
Best Local Similarity 42.6%; Pred. No. 1.1e-49;
Matches 123; Conservative 44; Mismatches 100; Indels 22; Gaps 8;

QY 17 RGALLALILARAGLKPESQBAAPLSGCGRRVTSRIVGGDAELGRPMWQSGRLWD 76
DB 3 RPAVPPLLLLLCGSORAKAATA-----CGPRMLNRMWGGQDTQSGEPWQVSIORNG 56

QY 77 SHVCGVSLLSHRWALTAACFCFETYSDLDPGSGMWVQFG--QLTSMPSFWSLQAYTRYFV 134
DB 57 SHFCGGLIAEOWVLTAACFCR---NTSETSLYQLLQARQLVQP----GPHAWYAR--V 107

```

```
QY 110 MYQFG--QLTSMPSFWSLQAVYTRFVSNIVLSRYL--GNSPYDIALVKLSAPVYTKHI 166
Db 53 EVKGAHQDLS-----YSDAKVST--LKDIIHPHSYLOEGSQGDIALQLSRPITFSRYI 106
QY 167 QPICQASTFEFENRTDCWVTGWGVIKEDALPSHTLQEVQVAIINNSMCHLF--LK 223
Db 107 RPICLPAANASFPNGLHCTVTGWHVAPSVLLTPKPLQQLLEVPLISRETCLNIDAK 166
QY 224 YSRKDIIFGDMVCAGNAQGGKDACFGDSGGPLACNKLWYQIGVSVGWGCGRPNRPGV 283
Db 167 PEERHFVQEDMVCAGYVSGGKDACQDGGSGPLSCPVGLWYLTGIVSGWDGACGARNRPGV 226
QY 284 YNNISHHFEWIO-----KLMAQSGMSQDDPSW-----PLFFPPLL 318
Db 227 YTLASSYASWISQKYTELQPRVVPQTQESQDNLCSHLAFSSAPAGQLLRPIFLPLG 286
QY 319 WALPLLGP 326
Db 287 LALGLLSP 294

RESULT 11
US-09-386-653A-9
; Sequence 9, Application US/09386653A
; Patent No. 6458564
; GENERAL INFORMATION:
; APPLICANT: Andrade-Gordon, Patricia
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jian-shen
; TITLE OF INVENTION: DNA encoding the novel human serine
; protease I
; FILE REFERENCE: ORT-1032
; CURRENT APPLICATION NUMBER: US/09/386,653A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion Protein
; OTHER INFORMATION: Of Protease T in a zymogen activation construct
US-09-386-653A-9
Query Match 30.7%; Score 550; DB 4; Length 315;
Best Local Similarity 40.3%; Pred. No. 3.3e-47;
Matches 123; Conservative 46; Mismatches 104; Indels 32; Gaps 10;

QY 14 MGARGA-----LLALLLAR-----AGLRKPESQEAAPLSGPCGRRVITSRIYGGED 60
Db 1 MDSKSSQKSRLLLLVSNLLCGQVSDYKDDDDVDAALAAPDD---DDKIVGGYA 57
QY 61 AELGRWPQGSRLWDSHVCVSLSHRWALTAACHFETYSDLSDPSCMMVQFG--QLTS 118
Db 58 LEEGWPQVSIQRNGSHPCGSGSLIAEQWLVLTAAHCFR---NTSETSLYQLLQARQLVQ 114
QY 119 MFSFWSLQAVYTRFVSNIVLSRYLGN--SPYDIALVKLSAPVYTKHIQICLQASTFE 177
Db 115 P-----GPHAWYAR--VRQVESNPLYCGTASSADVALVEAFVPTNYILPVCLPDPFSVI 168
QY 178 FENRTDCWVTGWGVIKEDALPSHTLQEVQVAIINNSMCHLFK-----YSFR-KDIPGD 233
Db 169 PETGMNCWVTGWSPEEDLLPEPRILQKLAVIDTPKCNLLYSKDTFPGYQPKTIKD 228
QY 234 MYCAGNAQGGKDACFGDSGGPLACNKLWYQIGVSVGWGCGRPNRPGVYTNISHHFEW 293
Db 229 MLCAGFEQKDKACKDGGSGPLVCLVGOSWLGAVISWGEGCARQNREGVIRVTAHNNW 288
QY 294 IQKLM 298
Db 289 IHRII 293
```

```
RESULT 12
US-09-386-642-11
; Sequence 11, Application US/09386642
; Patent No. 6420157
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jensen
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
; OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-11
```

```
Query Match 30.2%; Score 541.5; DB 4; Length 328;
Best Local Similarity 39.3%; Pred. No. 2.5e-46;
Matches 128; Conservative 51; Mismatches 98; Indels 49; Gaps 11;

QY 14 MGARGA-----LLALLLAR-----AGLRKPESQEAAPLSGPCGRRVITSRIYGGED 60
Db 1 MDSKSSQKSRLLLLVSNLLCGQVSDYKDDDDVDAALAAPDD---DDKIVGGYA 57
QY 61 AELGRWPQGSRLWDSHVCVSLSHRWALTAACHFETYSDLSDPSCMMVQFG--114
Db 58 LEAGWPQVSIYEGVHVHVCVSLSEQWVLSAAHCF-----PSEHKEAYEVKLG 109
QY 115 -QLTSMPSFWSLQAVYTRFVSNIVLSRYL--GNSPYDIALVKLSAPVYTKHIQICLQ 172
Db 110 HQDLS-----YSDAKVST--LKDIIHPHSYLOEGSQGDIALQLSRPITFSRIIRCLP 163
QY 173 ASFFEFENRTDCWVTGWGVIKEDALPSHTLQEVQVAIINNSMCHLF---LKYSFRKD 229
Db 164 AANASFPNGLHCTVTGWHVAPSVLLTPKPLQQLLEVPLISRETCLNIDAKPEPHF 223
QY 230 IFGDMVCAGNAQGGKDACFGDSGGPLACNKLWYQIGVSVGWGCGRPNRPGVYTNISH 289
Db 224 VQEDMVCAGYVSGGKDACQDGGSGPLSCPVGLWYLTGIVSGWDGACGARNRPGVYTLASS 283
QY 290 HFEWIO-----KLMAQSGMSQPD 307
Db 284 YASWISQKYTELQPRVVPQTQESQPD 309
```

```
RESULT 13
US-09-386-642-12
; Sequence 12, Application US/09386642
; Patent No. 6420157
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jensen
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
```

OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-12

Query Match 30.2%; Score 540.5; DB 4; Length 319;
Best Local Similarity 41.4%; Pred. No. 3.1e-46;
Matches 127; Conservative 43; Mismatches 98; Indels 39; Gaps 10;

QY 23 ALLARAGLRKP---ESQEAAPLSGCGRRVITSRIVGDEDAELGRWPMQGSRLWDSDV 79
DB 11 ALLTTTGGVDPYKDDDDAALAPFD---DDKIVGGYALEAGOWPMQVSVIYGVHV 67

QY 80 CGVSLSHRWALTAHCFETYSDLSDFS-----GMVQFG--QLTSMPSFWSLQAYTRY 132
DB 68 CGSLVSEQWLSAAHCF-----PSEHKAEAYEVLGAHQLDSD---YSEDAKVST- 114

QY 133 FVSNILSPRL-CNSPYDIALVKLSAPVYTKHIQICLOASTFFEFENRTDCWVTGWY 191
DB 115 -LKDIIPHPSYQSGSGDIALLOLSRPIITFSYRIPICLPANASFPNGLHCTVTGWGH 173

QY 192 IKEDEALPSHTLQEVQVAIINNMCNHLF---LKYSFRKIDFGDMVCAGNAOGGKDACF 248
DB 174 VAPSVLLTPKPLQQLVPLISRETCLNIDAKPEPHFVQEDMVCAGYVSGKDAQ 233

QY 249 GDSGGLACNKNGLWYQIGVSWGCGRRNRPGRVYTNISHHFEWIO-----KLMAQ 300
DB 234 GDSGGLSCPVBEGLWYLTGIVSGDAGCARNRPGVYTLASSYASWIOSKVTELQPRVFP 293

QY 301 SGMSQPD 307
DB 294 TQESQPD 300

RESULT 14

US-09-386-629-7
Sequence 7, Application US/09386629
Patent No. 6426199

GENERAL INFORMATION:

APPLICANT: Darrow, Andrew L.

APPLICANT: Qi, Jensen

APPLICANT: Andrade-Gordon, Patricia

TITLE OF INVENTION: Identification and Characterization of the complementary
FILE OF INVENTION: DNA encoding the novel human serine protease C-E

FILE REFERENCE: ORT-1030

CURRENT APPLICATION NUMBER: US/09/386,629

CURRENT FILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patent Ver. 2.0

SEQ ID NO 7

LENGTH: 317

TYPE: PRT

ORGANISM: Homo sapiens

US-09-386-629-7

Query Match 29.7%; Score 531.5; DB 4; Length 317;
Best Local Similarity 36.0%; Pred. No. 2.5e-45;
Matches 111; Conservative 57; Mismatches 115; Indels 25; Gaps 6;

QY 15 GARGALLALLARAGLRKPESQEAAPLSGCGRRVITSRIVGDEDAELGRWPMQGSRL 74
DB 13 GCLTFTSLLLATAIL---NAARIPVACPKPQOLNVRVVGEDSTOSEWPMVISIQ 69

QY 75 WDSHVCVGSLLSHRWALTAHCFETYSDLSDFS---GMVQFG--QLTSMPSFWSLQAYTRY 133
DB 70 NGTHCAGSLTSRWVITAAHCFK---DNLNKPVLFSVLLCA-----WQLGNPGRSQK 120

QY 134 VSNILSPRL---VLGNSPYDIALVKLSAPVYTKHIQICLOASTFFEFENRTDCWVTGW 189
DB 121 VGVAVVEPHVPSYQSGSGDIALLOLSRPIITFSYRIPICLPANASFPNGLHCTVTGWGH 180

QY 190 GYKDEALPSHTLQEVQVAIINNMCNHLF---LKYSFRKIDFGDMVCAGNAOGGKDACF 249
DB 181 GSIQDGVLPHPQTLQKLKVPIDSEVCSHLYWRGACQGPITEDMLCAGVLEGERDACLG 240

QY 250 DSGGFLACNKNGLWYQIGVSWGCGRRNRPGRVYTNISHHFEWIOKLM-----AQS 301
DB 241 DSGGFLACNKNGLWYQIGVSWGCGRRNRPGRVYTNISHHFEWIOKLM-----AQS 300

QY 302 QMSQPDPS 309
DB 301 GQALRAPDS 308

RESULT 15

US-09-907-794A-263
Sequence 263, Application US/09907794A
Patent No. 6635468

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

APPLICANT: Ashkenazi, Avi

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, A.

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth, J.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Mather, Jennie P.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas P.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William, I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/907,794A

CURRENT FILING DATE: 2001-07-17

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR FILING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR FILING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR FILING DATE: 1999-07-28

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR FILING DATE: 1999-09-08

PRIOR APPLICATION NUMBER: PCT/US99/20944

PRIOR FILING DATE: 1999-09-13

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/21547

PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/23089

PRIOR FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: PCT/US99/28214

PRIOR FILING DATE: 1999-11-29

PRIOR APPLICATION NUMBER: PCT/US99/28313

PRIOR FILING DATE: 1999-11-30

PRIOR APPLICATION NUMBER: PCT/US99/28564

PRIOR FILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/28565

PRIOR FILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/30095

PRIOR FILING DATE: 1999-12-16

PRIOR APPLICATION NUMBER: PCT/US99/30911

```
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 263
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-907-794A-263

Query Match      29.7%; Score 531.5; DB 4; Length 317;
Best Local Similarity 36.0%; Pred. No. 2.5e-45;
Matches 111; Conservative 57; Mismatches 115; Indels 25; Gaps 6;

QY 15 GARGALLALLARAGLRKPESQEAAPLSGPGCRRVITTSIVGGEDAELGRNFWQGSLEL 74
Db 13 GCLGTFSTLLLLASTAL---NAARIPVPACGKPPQLNRVVGEDSTDSWFWIVSIQK 69

QY 75 WDSHVCVSVLLSHRWALTAHCFETYSDLSDPGVMVQFQQLTSMFSFWSLQAYYTR-YF 133
Db 70 NGTHHCAGSLTTSRWVITAAHCFK--DNLNKPYLFSVLLGA-----WOLGNPGRSQK 120

QY 134 VSNITLSPR---YLGNSPYDIALVLSAPVYTKHIQPICLQASTFEFENRTDCWVTGW 189
Db 121 VGVAVVEPHVPYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPNTHCWISGW 180

QY 190 GYIXEDALPSPHTLQEVQVAIINNSMCHLFLKYSFRKDFGDMVCAGNAQGGKDACFG 249
Db 181 GSIQDGVLPHPQTLQKLVPIIDSEVCVSHLYWRGAGQGPITEDMLCAGYLEGERDACL 240

QY 250 DSGGPLACNKNGLWYQIGVSWGVGCGRPNGRPVYTNISHHFEWIOKLM-----AQS 301
Db 241 DSGGPLMCQVDGAWLLAGIISWEGECAERNRPVITSLSAHRSWVEKIVGVQVLRGQAQ 300

QY 302 GMSQPDPS 309
Db 301 GGALRAPS 308
```

Search completed: April 6, 2004, 14:14:13
Job time : 24 secs

GenCore version 5.1.1.6
 Copyright (c) 1993 - 2004 CompuGen Ltd.
 OM protein - protein search, using sw model
 Run on: April 6, 2004, 14:05:54 ; Search time 17 seconds
 (without alignments)
 1001.585 Million cell updates/sec

Title: US-09-787-844-2
 Perfect score: 1792
 Sequence: 1 RQGRQAGEANGARGAL.....PSWLLFFLLWALPLGPV 327

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues
 Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1728	96.4	314	1 TEST HUMAN	Q9Y6M0 homo sapien
2	1147	64.0	324	1 TEST MOUSE	Q9JHJ7 mus musculus
3	603	33.6	321	1 TRYX HUMAN	Q9NR22 homo sapien
4	580	32.4	343	1 PS58 HUMAN	Q16651 homo sapien
5	574	32.0	290	1 PR27 HUMAN	Q9BQR3 homo sapien
6	562.5	31.4	342	1 PS58 RAT	Q9ES87 rattus norv
7	561.5	31.3	342	1 PS58 MOUSE	Q9ESD1 mus musculus
8	556.5	31.1	311	1 TRYX MOUSE	Q9QLU7 mus musculus
9	544	30.4	273	1 TRYX SHEEP	Q9XSM2 ovis aries
10	543	30.3	811	1 TMS6 MOUSE	Q9DB10 mus musculus
11	531.5	29.7	217	1 B584 HUMAN	Q9GZM4 homo sapien
12	528.5	29.5	270	1 TRYX MERUN	P50342 meriones un
13	522	29.1	275	1 TRYX PIG	Q9N2D1 sus scrofa
14	520	29.0	306	1 B584 MOUSE	Q9ER10 mus musculus
15	515	28.7	275	1 TRB1 HUMAN	Q15661 homo sapien
16	514.5	28.7	638	1 KAL MOUSE	P26262 mus musculus
17	514	28.7	275	1 TMS2 HUMAN	P20231 homo sapien
18	513	28.6	638	1 KAL HUMAN	P20352 homo sapien
19	512	28.6	276	1 MCT6 MOUSE	P21845 mus musculus
20	511	28.5	275	1 TRYX CANFA	P15944 canis faml
21	511	28.5	638	1 KAL RAT	P14272 rattus norv
22	509.5	28.4	273	1 MCT7 RAT	P27435 rattus norv
23	509	28.4	811	1 TMS6 HUMAN	Q8U80 homo sapien
24	508.5	28.4	454	1 TMS3 HUMAN	P57727 homo sapien
25	507	28.3	273	1 MCT7 MOUSE	Q02844 mus musculus
26	505	28.2	453	1 TMS3 MOUSE	Q8KIT0 mus musculus
27	500	27.9	274	1 MCT6 RAT	P50343 rattus norv
28	499	27.8	275	1 TRYX HUMAN	P15157 homo sapien
29	490.5	27.4	435	1 TMS4 MOUSE	Q8VCAS mus musculus
30	489.5	27.3	418	1 HATT HUMAN	Q60235 homo sapien
31	487.5	27.2	455	1 TMS5 MOUSE	Q9ER04 mus musculus
32	483.5	27.0	625	1 FALL_HUMAN	P03951 homo sapien
33	478	26.7	437	1 TMS4_HUMAN	Q9NRS4 homo sapien

ALIGNMENTS

RESULT 1

ID	TEST HUMAN	STANDARD;	PRT;	314 AA.
AC	Q9Y6M0; Q9NG34; Q9P2V6;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Testisin precursor (EC 3.4.21.-) (Eosinophil serine protease 1) (ESP-1) (UNQ266/PRO303).			
GN	PRSS21 OR TEST1 OR ESP1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Eosinophil;			
RX	MEDLINE=99045401; PubMed=2626525;			
RA	Inoue M., Kanbe N., Kurosawa M., Kido H.;			
RT	"Cloning and tissue distribution of a novel serine protease esp-1 from human eosinophils.";			
RL	Biochem. Biophys. Res. Commun. 252:307-312(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 3).			
RX	MEDLINE=20068805; PubMed=10600542;			
RA	Inoue M., Isebe M., Itoyama T., Kido H.;			
RT	"Structural analysis of esp-1 gene (PRSS 21).";			
RL	Biochem. Biophys. Res. Commun. 266:564-568(1999).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RC	TISSUE=Cervical carcinoma;			
RX	MEDLINE=99323395; PubMed=10397266;			
RA	Hooper J.D., Nicol D.L., Dickinson J.L., Eyre H.J., Scarman A.L.,			
RT	Normyle J.F., Stuttgen M.A., Douglas M.L., Loveland K.A.,			
RL	Sutherland G.R., Antalis T.M.;			
RT	"Testisin, a new human serine proteinase expressed by premeiotic testicular germ cells and lost in testicular germ cell tumors.";			
RL	Cancer Res. 59:3199-3205(1999).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20461760; PubMed=11004480;			
RA	Hooper J.D., Bowen N., Marshall H., Cullen L.M., Sood R., Daniels R.,			
RT	Stuttgen M.A., Normyle J.F., Higgs D.R., Kastner D.L., Ogbourne S.M.,			
RL	Pera M.F., Jazwinska E.C., Antalis T.M.;			
RT	"Localization, expression and genomic structure of the gene encoding the human serine protease testisin.";			
RL	Biochim. Biophys. Acta 1492:63-71(2000).			
RN	[5]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=2887296; PubMed=12975309;			
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,			
RT	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,			
RL	Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.B., Heidens S.,			
RT	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,			
RL	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,			
RT	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,			

34	477.5	26.6	417	1	HEPS HUMAN	P05981 homo sapien
35	472.5	26.4	422	1	DESI HUMAN	Q9U152 homo sapien
36	468	26.1	430	1	TMS2_MOUSE	Q9JIG8 mus musculus
37	466	26.0	436	1	HEPS_MOUSE	C35453 mus musculus
38	459.5	25.6	492	1	TMS2_HUMAN	O15393 homo sapien
39	457.5	25.5	457	1	TMS5_HUMAN	Q9H363 homo sapien
40	455.5	25.4	415	1	ACRO_PIG	P08001 sus scrofa
41	455.5	25.4	810	1	PLMN_HUMAN	P00747 homo sapien
42	454.5	25.4	1069	1	ENTK_MOUSE	P97435 mus musculus
43	454	25.3	338	1	PLMN_HORSE	P80010 equus caball
44	452.5	25.3	436	1	ACRO_MOUSE	P23578 mus musculus
45	447	24.9	416	1	HEPS_RAT	Q05511 rattus norv

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guscini S., Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Hayashizaki A., Yoshida K., Hasegawa Y., Kawaji H., Kotsuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -!- FUNCTION: Could regulate proteolytic events associated with
CC testicular germ cell maturation.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC (Potential).
CC -!- TISSUE SPECIFICITY: Testis.
CC -!- DEVELOPMENTAL STAGE: Expressed in post-meiotic testicular germ
CC cells.
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- CAUTION: Ref.3 sequence differs from that shown due to a stop
CC codon in position 315.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/commence/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF304012; AAK29360.1; -;
DR EMBL: AY005145; AAG02255.1; -;
DR EMBL: AF176209; AAF64407.2; -;
DR EMBL: AF226710; AAF64428.2; -;
DR EMBL: AK006271; -; NOT_ANNOTATED_CDS.
DR HSSP: P00763; 1DPO.
DR MEROPS: S01.011; -;
DR MGD: MGI:1916698; Prrs21.
DR GO: GO:0005624; C-membrane fraction; IDA.
DR GO: GO:0004252; F-serine-type endopeptidase activity; IDA.
DR InterPro: IPR009003; Cys_Ser_trypsin.
DR InterPro: IPR001254; Peptidase_S1.
DR InterPro: IPR001314; Peptidase_S1A.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; TRYPSIN_DOM; 1.
DR PROSITE: PS02440; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR Hydroxylase; Serine protease; Glycoprotein; Signal; GPI-anchor; Zymogen;
KW Lipoprotein.
FT SIGNAL 1 21 POTENTIAL.
FT PROPEP 22 54 POTENTIAL.
FT CHAIN 55 298 TEST-SIN.
FT PROPEP 299 324 REMOVED IN MATURE FORM (POTENTIAL).
FT ACT_SITE 95 95 CHARGE RELAY SYSTEM (POTENTIAL).
FT ACT_SITE 147 147 CHARGE RELAY SYSTEM (POTENTIAL).
FT ACT_SITE 248 248 CHARGE RELAY SYSTEM (POTENTIAL).
FT DISULFID 46 167 POTENTIAL.
FT DISULFID 80 96 POTENTIAL.
FT DISULFID 181 254 POTENTIAL.
FT DISULFID 214 233 POTENTIAL.
FT DISULFID 244 272 POTENTIAL.
FT LIPID 298 298 GPI-anchor amidated asparagine
FT (Potential).
FT

FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 283 283 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 275 275 P -> H (IN REF. 3).
SQ SEQUENCE 324 AA; 36175 MW; 56DC59B84F3C3CD4 CRC64;
Query Match 64.0%; Score 1147; DB 1; Length 324;
Best Local Similarity 64.7%; Pred. No. 1.6e-95;
Matches 211; Conservative 39; Mismatches 60; Indels 16; Gaps 4;
QY 14 MGARGALLALL--LAPAGL-----RKPEQEAAPLSPGCGRRVITSRIVGGD 60
DB 1 MGARGKTLVPLVVVATAAALOSTYLVDPKPELQEPDLSGPGCHRTIPSRIVGGD 60
QY 61 AELGRWPGQSLRLWDSHVGVLLSHRWALTAHCFETYSYLSLSDSGWVQGLTSM 120
DB 61 AELGRWPGQSLRVGNHLCATLNRRLVWLTAAHCFQ--KD--NDPFDVTVQGLTSRP 117
QY 121 SFWSLQAYTRYFVSNLYLSPRYLGNSPYDIALVKLSAPVYTKHIQICLOASTFEFEN 180
DB 118 SLNWLAQSNRYQIEDIFLSPKISEQYNDIALKLSPPVYNNFIQICLLNSTYKFN 177
QY 181 RTDCWVTGMYIKEDALPSPHTLQVQVAIINNMCNHLFLKYSFRKDFGDMVCAGNA 240
DB 178 RTDCWVTGMYIKEDALPSPHTLQVQVAIINNMCNHLFLKYSFRKDFGDMVCAGTP 237
QY 241 QGGKACFCGDSGGPLACNKLWYQIGVSWGVCGRNRPVYTNISHHFEVQKLMQ 300
DB 238 EGGKACFCGDSGGPLACDQDTVWYGVWSGIGCGRNPVYTNISHHYVQSTWIR 297
QY 301 SGMSQDPSPPLFFFLWALPLGP 326
DB 298 NGLLRDPDVPVLLFLTLAWASSLLRP 323
RESULT 3
TRYG HUMAN STANDARD; PRT; 321 AA.
ID TRYNR2; Q9NR08; Q9UBB2;
AC Q9NR2; Q9NR08; Q9UBB2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Trypsin gamma precursor (EC 3.4.21.-) (transmembrane trypsinase).
GN TFSGL OR TMT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (VARIANTS GAMMA-1 AND GAMMA-2).
RX MEDLINE=20302813; PubMed=10843716;
RA Caughey G.H., Raymond W.W., Blount J.L., Hau L.W., Pallaro M.,
RA Wolters P.J., Verghese G.M.;
RT "Characterization of human gamma-tryptases, novel members of the
RT chromosome 16p mast cell tryptase and proctasin gene families.";
RL J. Immunol. 164:6566-6575(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99452974; PubMed=10521469;
RA Wong G.W., Tang Y., Feyfant E., Sali A., Li L., Li Y., Huang C.,
RA Friend D.S., Krilis S.A., Stevens R.L.;
RT "Identification of a new member of the tryptase family of mouse and
RT human mast cell proteases which possesses a novel COOH-terminal
RT hydrophobic extension.";
RL J. Biol. Chem. 274:30784-30793(1999).
RN [3]
RP SEQUENCE OF 220-321 FROM N.A.
RA Mittman S., Agnew W.S.;
RT "Organization and alternative splicing of CACNAH.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Membrane-anchored (Potential).
CC -!- TISSUE SPECIFICITY: Expressed in many tissues.

CC -!- POLYMORPHISM: There are two alleles; gamma-I and gamma-II which
 CC differ by 5 residues.
 CC -!- SIMILARITY: Belongs to peptidase family S1. Trypsin subfamily.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AF191031; AAF76457.1; -;
 DR EMBL; AF195508; AAF76458.1; -;
 DR EMBL; AF175759; AAF03697.1; -;
 DR EMBL; AF175522; AAF03695.1; -;
 DR EMBL; AF223563; AAG48852.2; -;
 DR HSP; P00763; 1DPO.
 DR MEROPS; S01.028; -;
 DR Gnew; HGNC:14134; TP8G1.
 DR InterPro; IPR009003; Cys_ser_trypsin.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PS00722; CHYMOTRYPSIN.
 DR PROSITE; PS00240; TRYPsin DOM; 1.
 DR PROSITE; PS00134; TRYPsin HIS; 1.
 DR PROSITE; PS00135; TRYPsin SER; FALSE NEG.
 DR HydroLase; Serine protease; Signal; Glycoprotein; Zymogen;
 KW Transmembrane; Polymorphism.
 KX SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 36 TRYPTASE GAMMA LIGHT CHAIN.
 FT CHAIN 38 321 TRYPTASE GAMMA HEAVY CHAIN.
 FT TRANSMEM 284 304 POTENTIAL.
 FT ACT_SITE 78 78 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 125 125 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 222 222 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 222 222 INTERCHAIN (POTENTIAL).
 FT DISULFID 63 79 BY SIMILARITY.
 FT DISULFID 159 228 BY SIMILARITY.
 FT DISULFID 192 210 BY SIMILARITY.
 FT DISULFID 218 246 BY SIMILARITY.
 FT CARBOHYD 85 85 N-LINKED (GLNAC...) (POTENTIAL).
 FT VARIANT 60 60 /FTid=VAR_012097.
 FT VARIANT 126 126 I -> M (IN GAMMA-II).
 FT VARIANT 132 132 S -> T (IN GAMMA-II).
 FT VARIANT 204 204 L -> I (IN GAMMA-II).
 FT VARIANT 288 288 L -> F (IN GAMMA-II).
 FT VARIANT 288 288 /FTid=VAR_012101.
 FT CONFLICT 160 160 W -> S (IN REF. 1).
 SQ SEQUENCE 321 AA; 33827 MW; PFF7B06E3C4A962D CRC64;
 Query Match 33.6%; Score 603; DB 1; Length 321;
 Best Local Similarity 42.9%; Pred. No. 1e-46;
 Matches 140; Conservative 40; Mismatches 98; Indels 48; Gaps 11;
 QY 13 AMGARGALLALLARAGLAKPESQEAAPLSGCGRRVIT---SRIVGGEDAEELGWPWQ 69
 DB 2 ALGACG-LLLLLAVPGVSLR-----TLQCGGRPOVSDAGRIVGGAAPAGAWPQ 52
 QY 70 GSLRLNWHVCGVLLSHRWALTAHCFEYSDLSDPGGMWQFQGL--TSMSPFSLQA 127
 DB 53 ASLRRLRHVCGVLLSPQWLTAAHCFSGSLNSD---YQVHLGELEITLSPHFSTVQ 109
 QY 128 YYTRYFVSNVYLSRYLGNISPYDIALVKLSAPVYTKHQPICLOASTFEFENRTDCWVT 187
 DB 110 II-----LHSSSGQPGTSGDIALVELSVPTLTLVCLPEASDPCFGICWVT 162
 QY 198 GWGIKEDALPSPHITQEVQVAIVNINSMCNHLFLKYSFRKIDFG-----DMVCAGN 239

Db 163 GWYTTREGFLPPPYSLREVKVSVDVETC-----RRDYFGGSGILPDMC--- 210
 QY 240 AQQGKDACGDSGGPLACNKNGLWYQIGVYVWGVCGRNRRPGVYTNISHHFEWIKLMA 299
 Db 211 ARGPGDACQDDSGPLVCVNGAWVQAGIVSWGCGCRNRRPGVYTRVPAVYNWIRRHIT 270
 QY 300 QSGMSQED-PSWPL---LSEPLLWAL 321
 Db 271 ASGGSSEGYRLPLLAGLFLPLGLLL 296
 RESULT 4
 PSS8 HUMAN
 ID PSS8 HUMAN STANDARD; PRT; 343 AA.
 AC Q16651; Q9UCA3;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Prostate precursor (EC 3.4.21.-).
 GN PRSS8.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Prostate;
 EX MEDLINE=95286644; PubMed=7768952;
 RA Yu J.X., Chao L., Chao J.;
 RT "Molecular cloning, tissue-specific expression, and cellular
 RT localization of human prostatic mRNA.";
 RL J. Biol. Chem. 270:13483-13489(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 EX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Tothiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Joquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE OF 45-64.
 RC TISSUE=Semen;
 EX MEDLINE=94308140; PubMed=8034638;
 RA Yu J.X., Chao L., Chao J.;
 RT "Prostatein is a novel human serine proteinase from seminal fluid.
 RT Purification, tissue distribution, and localization in prostate
 RT gland.";
 RL J. Biol. Chem. 269:18843-18848(1994).
 CC -!- FUNCTION: Possesses a trypsin-like cleavage specificity.
 CC -!- SUBUNIT: Heterodimer of two chains, light and heavy, held by a
 CC disulfide bond.
 CC -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. SECRETED AFTER CLEAVAGE OF
 CC ITS C-TERMINUS.
 CC -!- TISSUE SPECIFICITY: Found in prostate, liver, salivary gland,
 CC kidney, lung, pancreas, colon, bronchus and renal proximal tubular

CC cells. In the prostate gland it may be synthesized in epithelial
 CC cells, secreted into the ducts, and excreted into the seminal
 CC fluid.
 CC -!- SIMILARITY: Belongs to peptidase family S1.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; L41351; AAC41759.1; -;
 DR EMBL; U33446; AAB19071.1; -;
 DR EMBL; BC001462; AAH01462.1; -;
 DR PIR; A57014; A57014.
 DR HSP; P00763; LDPO.
 DR MEROPS; S01.159; -;
 DR Genew; HGNC:9491; PRSS8.
 DR MIM; 600823; -;
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0005886; C:plasma membrane; TAS.
 DR GO; GO:0008236; F:serine-type peptidase activity; TAS.
 DR InterPro; IPR009003; Cys_Ser_trypsin.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PRO0722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolyase; Serine protease; Zymogen; Signal; Glycoprotein;
 KW Transmembrane.
 FT SIGNAL 1 29 POTENTIAL.
 FT PROPEP 30 32 ACTIVATION PEPTIDE.
 FT CHAIN 33 44 PROSTATIN LIGHT CHAIN.
 FT CHAIN 45 322 PROSTATIN HEAVY CHAIN.
 FT PROPEP 323 343 POTENTIAL.
 FT TRANSMEM 320 340 POTENTIAL.
 FT DOMAIN 45 286 SERINE PROTEASE.
 FT DISULFID 37 154 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 70 86 BY SIMILARITY.
 FT DISULFID 168 244 BY SIMILARITY.
 FT DISULFID 201 223 BY SIMILARITY.
 FT DISULFID 234 262 BY SIMILARITY.
 FT ACT_SITE 85 85 CHARGE RELAY SYSTEM.
 FT ACT_SITE 134 134 CHARGE RELAY SYSTEM.
 FT ACT_SITE 238 238 CHARGE RELAY SYSTEM.
 FT CARBOHYD 159 159 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 343 AA; 36431 MW; 98DD6447F5A8C1B2 CRC64;
 Query Match 32.4%; Score 580; DB 1; Length 343;
 Best Local Similarity 40.6%; Pred. No. 1.3e-44;
 Matches 146; Conservative 47; Mismatches 107; Indels 60; Gaps 14;
 QY 3 ORGROAAGEAMGARGALLALLARAGLRKPESEAPLSPGCGRRVITTSRIVGDEAE 62
 DB 3 QKGVLPQO-ICA-VAIILYLGLRSG-TGEGREA-----PCG-VAPOARITGSSAV 52
 QY 63 LGRWPQGSRLWDHVGCVSLLSHRWALTAAHCFETVSDLSDDS-----GMVQFG--Q 115
 DB 53 AGQWPQVQSVITGVHVCGLSVSEQVLSAAHCF-----PSEHKEAYEVKLGAAHQ 104
 QY 116 LQSMPSFWSLQAVYTRYFVSNLYLSPRYL-GNSPVDIALVKLSAPVYTKHPTQICLOAS 174
 DB 105 LDS-----YSEDKAVST-LKDIPIHPSYLOEGSGDIALQLSRPITTSRIVRIPCIPAA 158
 QY 175 TFEFENRTDQWVGWYIKEDALPSPTLQEVQVAIINNSMCHLF---LKYSRKDIF 231
 DB 159 NASFPNGLHCTVGTGWGHVAPSVSLTPKPLQQLQLEVPILSRCTCNCLYNIDAKPEEPHFVQ 218

QY 232 GDMVCAAGNAGGKDACFGDSGGPLACNKNGLWYQIGVSWGVGCGRPNGPVYTNLSHF 291
 DB 219 EDWVCAGYVEGGKDACGDSGGPLSCPVEGLWYLVGIVSGDACGARNRPGVYTLASSVA 278
 QY 292 EMTQ-----KLMAQSGMSQDPDSW-----PLLPFLWALPLLP 326
 DB 279 SWIQSVTELOPRVVPQTESQPSDNLGSHLAFSSAPAGLRFLFLPLGLGLGLSP 338
 RESULT 5
 PR27_HUMAN STANDARD; PRT; 290 AA.
 ID PR27_HUMAN Q9BQR3;
 AC Q9BQR3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Pantothenase precursor (EC 3.4.21.-) (Marapsin) (Channel-activating
 DE protease 2) (CAPH2).
 GN PRSS27 OR MEN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Fortunato M., Dando P.M., Rawlings N.D., Barrett A.J.;
 RT "Cloning, sequencing and expression of marapsin, a human serine
 RT proteinase.",
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Okaze H., Havaashi A., Kozuma S., Saito T.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22439795; PubMed=12441343;
 RA Bhagwandin V.J., Hau L.W.-T., Mallen-St Clair J., Wolters P.J.,
 RA Caughey G.H.;
 RT "Structure and activity of human pantothenase, a novel tryptic serine
 RT peptidase expressed primarily by the pancreas.",
 RL J. Biol. Chem. 278:3363-3371(2003).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed predominantly in the pancreas.
 CC -!- PTM: N-glycosylated.
 CC -!- SIMILARITY: Belongs to peptidase family S1.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AJ306593; CAC35467.1; -;
 DR EMBL; AB056161; BAB85497.1; -;
 DR EMBL; AY030095; AAK38168.1; -;
 DR HSP; P00734; IUVS.
 DR MEROPS; S01.074; -;
 DR Genew; HGNC:15475; PRSS27.
 DR MIM; 608018; -;
 DR InterPro; IPR009003; Cys_Ser_trypsin.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PRO0722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolyase; Serine protease; Zymogen; Signal; Glycoprotein.
 FT SIGNAL 1 22 POTENTIAL.
 FT PROPEP 23 34

```
FT CHAIN 35 290 PANCREASIN.
FT DOMAIN 35 277 SERINE PROTEASE.
FT ACT_SITE 75 75 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 124 124 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 229 229 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 60 76 BY SIMILARITY.
FT DISULFID 158 235 BY SIMILARITY.
FT DISULFID 191 214 BY SIMILARITY.
FT DISULFID 225 253 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 290 AA; 31940 MW; 67BDC93EC70BFF7B CRC64;

Query Match 32.0%; Score 574; DB 1; Length 290;
Best Local Similarity 42.8%; Pred. No. 3.7e-44;
Matches 123; Conservative 44; Mismatches 100; Indels 22; Gaps 8;

QY 17 RGALLALLARAGLRKPKSQEAAPLSPGCGRRVITSRIVGDEDAELGRWPQGSRLRLWD 76
Db 3 RPAAPVLLLLLCFGSQRAKAATA-----CGRPRMLNRWVGQDTQEGEPWPQVSIQNG 56

QY 77 SHVGVSLLSHRWALTAHCFETYSLDSPSGMWVQFG--QLTSMPSFWSLQAYTRYFV 134
Db 57 SHFCGGSLLAEQWVLTAAHCFER---NTSETSLYQVLLGARQLVQP---GPHAMVYAR--V 107

QY 135 SNLYLSPRYLGN-SPYDIALVKLSAPVYTKHIQPICLQASTFEPENRDTDCWVTGWGVIK 193
Db 108 RQVESNPLVQGTASSADVALVEAPVPTNVLPLVCLPDPSPVIFETGNVCHWTGWSPS 167

QY 194 EDALPSPTLQEVQVAIINNSMCHFLK---YSFR-KDIFGDMVVCAGNAOGKACFG 249
Db 168 EEDLLPEPRILQKLVPIIDTPKCNLLYSKDTFEGYQPKTKINDMLCAGFEGKDKACKG 227

QY 250 DSGGGLACNKGWYQIGVGVSWGVGGGRPNRPGVTVNISHHFEWIOKLM 298
Db 228 DSGGGLVCLVQGSWQVLSWEGGCARQNPQVTVIRTAHNWIIIRII 276
```

```
RESULT 6
PSS8 RAT STANDARD; PRT; 342 AA.
AC Q9ES8; Q9ER01;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Proctasin precursor (SC 3.4.21.-).
GN PSS8.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Adachi M., Kitamura K., Miyoshi T., Tomita K.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RA Wang C.;
RL "Molecular cloning and expression of rat proctasin.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Possesses a trypsin-like cleavage specificity (By
CC similarity).
CC -1- SUBUNIT: Heterodimer of two chains, light and heavy, held by a
CC disulfide bond (By similarity).
CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND. SECRETED AFTER CLEAVAGE OF
CC ITS C-TERMINUS (BY SIMILARITY).
CC -1- SIMILARITY: Belongs to peptidase family S1.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
```

```
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch)
-----
CC ENBL; AB017638; BAB20281.1; -
CC ENBL; AF202076; AAC32641.1; -
CC HSPF; P00734; IUVS
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SMC0020; TRYD_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Zymogen; Signal; Glycoprotein;
KW Transmembrane.
FT SIGNAL 1 29 POTENTIAL.
FT PROPEP 30 32 ACTIVATION PEPTIDE (BY SIMILARITY).
FT CHAIN 33 44 PROSTATIN LIGHT CHAIN.
FT CHAIN 45 322 PROSTATIN HEAVY CHAIN.
FT PROPEP 323 342 BY SIMILARITY.
FT TRANSMEM 320 340 POTENTIAL.
FT DOMAIN 45 286 SERINE PROTEASE.
FT DISULFID 37 154 INTERCHAIN (BY SIMILARITY).
FT DISULFID 70 86 BY SIMILARITY.
FT DISULFID 168 244 BY SIMILARITY.
FT DISULFID 201 223 BY SIMILARITY.
FT DISULFID 234 262 BY SIMILARITY.
FT ACT_SITE 85 85 CHARGE RELAY SYSTEM (BY SIMILARITY)*
FT ACT_SITE 134 134 CHARGE RELAY SYSTEM (BY SIMILARITY)*
FT ACT_SITE 238 238 CHARGE RELAY SYSTEM (BY SIMILARITY)*
FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 17 17 I -> V (IN REF. 1).
FT CONFLICT 292 292 A -> V (IN REF. 1).
SQ SEQUENCE 342 AA; 36843 MW; SEDIAF0SD9213B98 CRC64;

Query Match 31.4%; Score 562.5; DB 1; Length 342;
Best Local Similarity 38.1%; Pred. No. 4.9e-43;
Matches 131; Conservative 53; Mismatches 93; Indels 67; Gaps 11;

QY 20 LLLALLARAGLRKPKSQEAAPLSPGCGRRVITSRIVGDEDAELGRWPQGSRLRLWD 79
Db 19 LLILQLQSRIG---ADGTEAS-----CG-AVIFRTGGSAKPGQWPQVSYTYNGVHV 69

QY 80 CGVSLLSHRWALTAHCFETYSLDSPSGMWVQFG--QLTSMPSFWSLQAYTRYFVSN- 136
Db 70 CGGSLVSNQWVWSAAHCFPREHSKEE---YEVKLGARHQLDSF-----SND 111

QY 137 --IVLSPRYLGNPY-----DIALVKLSAPVYTKHIQPICLQASTFEPENRDTDCWVT 187
Db 112 IVWHTVAQIISHSYREEGSQGDIALRLSSPVTFYSYIRIPICLPAAANAGFPNGLHCTVT 171

QY 188 GWGIKEDALPSPTLQEVQVAIINNSMCHFLKYSFRK---IFGDMVVCAGNAOGK 244
Db 172 GWGHVAPSVLSQTPRPLQQLLEVLPLISRETCSCLYNINAVPEEPTIQDMLCAGYVKGK 231

QY 245 DACFGDSGGPLACNKGWYQIGVGVSWGVGGGRPNRPGVTVNISHHFEWIO------K 296
Db 232 DACQDSGGPLSCPIDGLWYLAGIVSWGDACGAPNREGVYTLTSTYASWIIHHVAELQPR 291

QY 297 LMAQSGMSQDPF-----SWPLFFPPLLWALPL 323
Db 292 AVPTQESQDPDGLCHNHHPVFNLAQAQKLSRPLFLPLSLTLGL 335

RESULT 7
PSS8 MOUSE
ID PSS8 MOUSE STANDARD; PRT; 342 AA.
AC Q9RSD1.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
```

DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Proteasins precursor (EC 3.4.21.-) (Channel activating protease 1).
 GN PRS8 OR CAPI.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20235202; PubMed=10770960;
 RA Vuagniaux G., Vallet V., Jaeger N.F., Pfister C., Bens M., Farman N.,
 RA Coutois-Couty N., Vandewalle A., Rossier B.C., Hummler E.;
 RT "Activation of the aniloride-sensitive epithelial sodium channel by
 RT the serine protease mCAP1 expressed in a mouse cortical collecting
 RT duct cell line".
 RL J. Am. Soc. Nephrol. 11:828-834 (2000).
 CC -!- FUNCTION: Possesses a trypsin-like cleavage specificity (By
 CC similarity). Activates amiloride-sensitive sodium channels.
 CC -!- SUBUNIT: Heterodimer of two chains, light and heavy, held by a
 CC disulfide bond (By similarity).
 CC -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. SECRETED AFTER CLEAVAGE OF
 CC ITS C-TERMINUS (BY SIMILARITY).
 CC -!- SIMILARITY: Belongs to peptidase family S1.
 CC -!- CAUTION: Ref.1 sequence differs from that shown due to a
 CC frameshift in position 339.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements/>
 CC or send an email to license@ebi.ac.uk).
 CC
 CC EMBL; AF189613; AAG17054.1; ALT_FRAME.
 DR HSP; P00734; IUVS.
 DR MEROPS; S01.158; -.
 DR MGD; MGI:1923810; Prrs8.
 DR InterPro; IPR009003; Cys_Ser_trypsin.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00240; TRYPsin_DOM; 1.
 DR PROSITE; PS00134; TRYPsin_HIS; 1.
 DR PROSITE; PS00135; TRYPsin_SER; 1.
 DR Hydrolase; Serine protease; Zymogen; Signal; Glycoprotein;
 KW Transmembrane.
 FT SIGNAL 1 29 POTENTIAL.
 FT PROPEP 30 32 ACTIVATION PEPTIDE (BY SIMILARITY).
 FT CHAIN 33 44 PROSTATIN LIGHT CHAIN.
 FT CHAIN 45 322 PROSTATIN HEAVY CHAIN.
 FT PROPEP 323 342 BY SIMILARITY.
 FT TRANSMEM 320 340 POTENTIAL.
 FT DOMAIN 45 286 SERINE PROTEASE.
 FT DISULFID 37 154 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 70 86 BY SIMILARITY.
 FT DISULFID 168 244 BY SIMILARITY.
 FT DISULFID 201 223 BY SIMILARITY.
 FT DISULFID 234 262 BY SIMILARITY.
 FT ACT_SITE 85 85 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 134 134 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 238 238 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT CARBOHYD 110 110 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 159 159 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 342 AA; 36729 MW; 0620D98ED187D0F CRC64;
 Query Match 31.3%; Score 561.5; DB 1; Length 342;
 Best Local Similarity 37.9%; Pred. No. 6e-43; 88; Indels 71; Gaps 13;
 Matches 132; Conservative 57; Mismatches 88;
 20 LLLALLARAGKPEQAPSLGCGRRVITSGEDAEGLRWPMWGSLRLWDSHV 79

Db 17 ILLGLGSGIR-ADGTEAS-----CG-AVTPRTGGSAKPGQWPMQVITVDGNEV 69
 Qy 80 CGVSLLSHRWALTAAHCF-----ETYSLSDSPSGMWQFG--QLTSMPSFWSLQAYYTR 131
 Db 70 CGGSLVSNKVVSAAHCFPREHREAYE-----VKGAGHQLDS-----YSN 110
 Qy 132 YFVSNLYLSRYLGNSPY-----DIALVKLSAPVYTKHIQICLOASTFEFENRTDC 184
 Db 111 DTV--VHTVAQIITHSSVREBSQGGDIATIRUSSPVTFSYIRPICLPANASFPNGLHC 168
 Qy 185 WYTGWGYIKEDBALSPHTLQEVQVAIINNSMNLFLKYSRKH---IFGDMVCAGNAQ 241
 Db 169 TVTGWGHVAPSVLQTPRLQQLVPLISRETSCLYNINAVPEBPHITQQDMLCAGYVK 228
 Qy 242 GKKDACFGSGGGLACNKLWYQIVGVSNGVCGCRPNRPGVYTNLISHFEWIQ----- 295
 Db 229 GKKDACQGGSGGLSCPMEGIYLAGIVSWGACGAPNRPVYTTLTSTVASHHHVAEL 288
 Qy 296 --KLMAQSGMSOPD-----PSW-----PLLPPLLWALPLL 324
 Db 289 QRVVPTQESQPDGHLCHNHHPVFSAAAPKLLRPVLPFLGLTGLLL 336
 RESULT 8
 TRYQ MOUSE STANDARD; PRT; 311 AA.
 AC QSQUT7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 18-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Trypsin gamma precursor (EC 3.4.21.-) (Transmembrane trypsinase).
 GN TPSG1 OR TMT.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV, and BALB/c;
 RX MEDLINE=99452974; PubMed=10521469;
 RA Wong G.W., Tang Y., Peyfant E., Sali A., Li L., Li Y., Huang C.,
 RA Friend D.S., Kzilis S.A., Stevens R.L.;
 RT "Identification of a new member of the trypsinase family of mouse and
 RT human mast cell proteases which possesses a novel COOH-terminal
 RT hydrophobic extension".
 RL J. Biol. Chem. 274:30784-30793 (1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Tomshyuk S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters K.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Viallano D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -!- SUBCELLULAR LOCATION: Membrane-anchored (Potential).
 CC -!- TISSUE SPECIFICITY: Expressed in many tissues.

```

CC -!- SIMILARITY: Belongs to peptidase family S1. Trypsin subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF175760; AAF03698.1; -
DR EMBL; AF175523; AAF03696.1; -
DR EMBL; BC052325; AAH52325.1; -
DR HSP; P20231; IAAO.
DR MEROPS; S01.028; -
DR MGD; MGI1349391; Tpsgl.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR EMBL; AF175523; AAF03696.1; -
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; FALSE NEG.
KW Hydrolyase; Serine protease; Signal; Glycoprotein; Zymogen;
KW Transmembrane.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 28 TRYPTASE GAMMA LIGHT CHAIN.
FT CHAIN 30 311 TRYPTASE GAMMA HEAVY CHAIN.
FT TRANSMEM 277 297 POTENTIAL.
FT ACT_SITE 70 70 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 117 117 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 214 214 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 18 137 INTERCHAIN (POTENTIAL).
FT DISULFID 55 71 BY SIMILARITY.
FT DISULFID 151 220 BY SIMILARITY.
FT DISULFID 184 202 BY SIMILARITY.
FT DISULFID 210 238 BY SIMILARITY.
FT CARBOHYD 77 77 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 311 AA; 32656 MW; 7FC9D6F6A2A8808 CRC64;
Query Match 31.18; Score 556.5; DB 1; Length 311;
Best Local Similarity 39.84; Pred. No. 1.5e-42;
Matches 132; Conservative 39; Mismatches 102; Indels 59; Gaps 10;
Qy 13 AMGARGALLALLARAGLRKPESQEAAPLSGPGRRVITSRVGCGEDAEELGRWPQGSLL 72
Db 2 ALGNCGL-LFLAVSGCGHPQVNSG-----SRVGGHAPAGTWPQASL 47
Qy 73 RLMDSHVGVVLSHRWALTAACHFYETYSIDSPSGMWVQFGLTSPMSFWSLQAYTRY 132
Db 48 RLKHVHVCGSLSPWVLTAAHCFSGVNSSD---YQVHLGELT----- 89
Qy 133 FVSNIVLSR-----YLGN-----SPYDALVKLSAPVTVYTKHIQICLQASTFEF 178
Db 90 ----VTLSPHSTVKRIIMVTGPPGPGSGDIALVQLSPVALSQVPCVLPESADP 145
Qy 179 ENRTDCVWTGMYIKEDALPSPTLQEVQVAINNSMCHLFLKYSFRKIDFGMWVAG 238
Db 146 YPGMQCVWTGMYTGEGLKPPVNLQEAQVSVVVKVTCQAVNSPN-GSLIQDMLC-- 202
Qy 239 NAQGGKACFGDSGGPLACKNGIWLQIGVVSNGVCGGRNRPQVVTNISHHPEWIKLM 298
Db 203 -ARGPGACQDDSGPLVQVAGTWQAGVVVSGCGRDPGQVTVARVAYVNVVHHHI 261
Qy 299 AQSGMS--QPDPSWPL---LFFPLMALPLLG 325
Db 262 PEAGSGMQGLPWPAPLLAALFWPSLFLVLSV 293

```

RESULT 9
TRYT_SHEEP

```

ID TRYT_SHEEP STANDARD; PRT; 273 AA.
AC Q9XSM2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Trypsase 2 precursor (BC 3.4.21.59).
OS Ovis aries (Sheep).
OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Abomasum;
RX MEDLINE=20308142; PubMed=10848900;
RA Pemberton A.D., McLeese S.M., Huntley J.F., Collie D.D.S.,
RA Scudamore C.L., McQueen A.R., Wallis A.F., Miller H.R.P.;
RT "cDNA sequence of two sheep mast cell tryptases and the differential
RT expression of trypsin and sheep mast cell proteinase-1 in lung,
RT dermis and gastrointestinal tract.";
RT Clin. Exp. Allergy 30:818-832(2000).
CC -!- FUNCTION: Trypsin is the major neutral protease present in mast
CC cells and is secreted upon the coupled activation-degranulation
CC response of this cell type.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but
CC with more restricted specificity than trypsin.
CC -!- SUBUNIT: Homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Released from the secretory granules upon
CC mast cell activation.
CC -!- SIMILARITY: Belongs to peptidase family S1. Trypsin subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Y18224; CAB41989.1; -
DR HSP; P20231; IAAO.
DR MEROPS; S01.143; -
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Serine protease; Signal; Glycoprotein; Zymogen.
FT SIGNAL 1 18 POTENTIAL.
FT PROPEP 19 28 ACTIVATION PEPTIDE (BY SIMILARITY).
FT CHAIN 29 273 TRYPTASE 2.
FT ACT_SITE 72 72 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 119 119 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 222 222 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 57 73 BY SIMILARITY.
FT DISULFID 153 228 BY SIMILARITY.
FT DISULFID 186 209 BY SIMILARITY.
FT DISULFID 218 246 BY SIMILARITY.
FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 273 AA; 30288 MW; D59BA79218C3E67D CRC64;
Query Match 30.44; Score 544; DB 1; Length 273;
Best Local Similarity 40.54; Pred. No. 1.7e-41;
Matches 118; Conservative 46; Mismatches 93; Indels 34; Gaps 10;
Qy 20 LLLALLARAGLRKPESQEAAPLSGPGRRVITSRVGCGEDAEELGRWPQGSRLWDS-- 77
Db 5 LALALLSLV-----SAPAPQALQR---SGIIGKEAPGSRWPQVSLAVRQYW 53

```



```
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Repeat; Signal-anchor; Transmembrane;
KW Glycoprotein.
FT DOMAIN 1 59 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 60 80 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT ACT_SITE 81 811 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 213 336 CUB 1.
FT DOMAIN 323 440 CUB 2.
FT DOMAIN 445 477 LDL-RECEPTOR CLASS A 1.
FT DOMAIN 478 514 LDL-RECEPTOR CLASS A 2.
FT DOMAIN 518 555 LDL-RECEPTOR CLASS A 3.
FT DOMAIN 565 799 SERINE PROTEASE.
FT ACT_SITE 617 617 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 668 668 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 762 762 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT CARBOHYD 138 138 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 184 184 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 216 216 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 433 433 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 453 453 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 518 518 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 690 690 P -> PP (IN REF. 2).
SQ SEQUENCE 811 AA; 90978 MW; 32EB3E7C3127801B CRC64;

Query Match
Best Local Similarity 30.3%; Score 543; DB 1; Length 811;
Matches 105; Conservative 41.2%; Pred. No. 7.3e-41;
Mismatches 83; Indels 14; Gaps 7;

Qy 46 CGRVITSRIVGGEDAEGLRWPGQSLRLWDSHVGVLSLHRAWLTAACHFTYSDLSL 105
Db 568 CGLGGLSSRIYVGGVTSSEGEWQASLQIRGHICGALIAADRWVTAACHFQEDS-MAS 626
Qy 106 PSGMVQFGOLTSMPFSWLSQAYVTRVYFVSNIVLSRYLGNLS-PYDIALVKLSAPVYTK 164
Db 627 PKLWTVFLGKM-RQNSRPGEVSEFK---VSRLEFHPYHEEDSDYDVALQLDHPVYGA 582
Qy 165 HIQPICLAQSTFEFENRTDCWVTGWGVIKEDALPSPHTLOEVQVVAIINNSMCMHLFLKY 224
Db 683 TVRPVCLPARSHFPEQCHCWITGWG--AQREGPVSNLTQKVDQLVQDLGSE----- 735
Qy 225 SFRKDIFDGMVVCAGNAGGKDACFGDSGGFLACNK-NGLVQIQLGVVSGVGGGRNRPGV 283
Db 736 AYRYQVSPRLCAGYRKGDACQGDGGFLVCRFPSEGRWFLAGLVSWGLGCGRPNFFGV 795
Qy 284 YTNISHFEWIKLM 298
Db 796 YTRVTRVINNIQVL 810

RESULT 11
BSS4 HUMAN STANDARD; PRT; 317 AA.
ID BSS4 HUMAN
AC Q9GZNA; C43342;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Brain-specific serine protease 4 precursor (EC 3.4.21.-) (BSSP-4)
DE (SP001LA).
DE GN PRSS22 OR PRSS26 OR BSSP4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Mitsu S., Okui A., Kominami K., Yamaguchi N.;
RT "Cloning and characterization of a human brain-specific serine
protease, hBSSP-4."
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
```

```
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RA Wong G.W., Stevens R.L.;
RT "Identification of a new member of the chromosome 16 family of serine
proteases."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
MEDLINE=22389257; PubMed=12477932;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haileh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Souffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences".
Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).
RN [4]
RP SEQUENCE OF 47-317 FROM N.A.
RA Ricke D.O., Bruce D., Mundt M., Doggett N., Munk C., Saunders E.,
Robinson D., Jones M., Buckingham J., Chasteen L., Thompson S.,
Goodwin L., Bryant J., Tesmer J., Meincke L., Longmire J., White S.,
Ueng S., Tatum O., Campbell C., Fawcett J., Deaver L.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@sib-sib.ch).
CC
CC EMBL; AB010779; BAB20263.1; -
CC EMBL; AF321182; AAG35070.1; -
CC EMBL; BC009726; AA09726.1; -
CC EMBL; AC003965; AAB93671.1; -
CC HSP; P00763; LDPO.
CC MEROPS; S01.252; -.
CC Genew; HGNC:14368; PRSS22.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SMO0020; Tryp_SPC; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Signal.
FT SIGNAL 1 32 POTENTIAL.
FT CHAIN 33 317 BRAIN-SPECIFIC SERINE PROTEASE 4.
FT ACT_SITE 90 90 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 141 141 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 242 242 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 75 91 BY SIMILARITY.
FT DISULFID 175 248 BY SIMILARITY.
FT DISULFID 208 227 BY SIMILARITY.
FT DISULFID 238 266 BY SIMILARITY.
```



```

FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 47 47 L -> M (IN REF. 4).
SQ SEQUENCE 317 AA; 33731 MW; E2A123BC86E79935 CRC64;

Query Match
Best Local Similarity 29.7%; Score 531.5; DB 1; Length 317;
Matches 111; Conservative 57; Mismatches 115; Indels 25; Gaps 6;

QY 15 GARGALLALLIARAGLRKPKSQEAAPLSGCGRRVITSRVGVGDEALGRLWPGQSLRL 74
DQ 13 GCLGFTFTLLIATAIL--NAARIPVPACGPKQQLNRVVGGEDSTDESWPVIIVSIQK 69
QY 75 WDSHVGVSLSHRWALTAHCFEYISDLSPSGMWVQFGLTSMPSFWSLQAYYTR-YP 133
DQ 70 NGTHCAGSLTSRVITTAHCFK--DNENRYPVSVLLGA-----WQJNPGSRQK 120
QY 134 VSNYILSPR---YLGNSPYDIALVKLSAPVYTKHQIPICLOASTFEFENETDCWVTGW 189
DQ 121 VGVAWVEHPVYVSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPNTHCWISGW 180
QY 190 GYKEDALPSHTLOEQVOVAIINNSMCNHLFLKYSFKDIFGDMVCGNAGGKDACFG 249
DQ 181 GSIQGVFLPHPTQIKUKVPIIDSEVCVSHLYWRGAGGPITEDMVCAGYLEGERDACL 240
QY 250 DSGGLACNKGMLWQIGVSGVCGGRNRPVGVYTNISHHFEWIKLM-----AQS 301
DQ 241 DSGGLMCGVQDGAWLAGIISWGECAERNRPVGVYISLSAHSWVKIKVQVQLRGRAQG 300
QY 302 GMSQDPDS 309
DQ 301 GGLSAPS 308

RESULT 12
TRYT_MERUN
ID TRYT_MERUN STANDARD; PRT; 270 AA.
AC PS0342;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Mast cell tryptase precursor (EC 3.4.21.59).
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OX NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGS/SEA; TISSUE=Intestine;
RX MEDLINE=95366971; PubMed=7639711;
RA Murakumo Y., Ide H., Itoh H., Tomita M., Kobayashi T.,
RA Maruyama H., Horii Y., Nawa Y.;
RT "Cloning of the cDNA encoding mast cell tryptase of Mongolian gerbil,
RT Meriones unguiculatus, and its preferential expression in the
RT intestinal mucosa.";
RL Biochem. J. 309:921-926(1995).
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but
CC with more restricted specificity than trypsin.
CC -!- SIMILARITY: Belongs to peptidase family S1. Trypsin subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D31789; BAA06598.1; -.
DR PIR; S56160; S56160.
DR HSRP; P20231; IAAO.
DR MEROPS; S01.143; -.
DR InterPro; IPR009003; Cys_Ser_trypsin.

```

```

DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Signal; Glycoprotein.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 270 MAST CELL TRYPTASE.
FT ACT_SITE 69 69 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 116 116 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 219 219 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 54 70 BY SIMILARITY.
FT DISULFID 150 225 BY SIMILARITY.
FT DISULFID 183 206 BY SIMILARITY.
FT DISULFID 215 243 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 270 AA; 30166 MW; 1BE102DB86943401 CRC64;

Query Match
Best Local Similarity 29.5%; Score 528.5; DB 1; Length 270;
Matches 118; Conservative 36; Mismatches 92; Indels 45; Gaps 9;

QY 20 LLLALLARAGLRKPKSQEAAPLSGCGRRVITSRVGVGDEALGRLWPGQSLR---LW 75
DQ 5 LLLAFLFSLMRSPLCQEWG-----IVGGEAPGNKWPQVSLRANETW 50
QY 76 DSHVCGVSLSHRWALTAHCFEYISDLSPSGMWVQFGLTSMPSFWSLQAYYTRYF-- 133
DQ 51 -RHFCGSLHPQWLVLTAAHC--VGPTIADPNKVRVQ-----LRKQYLYYHDH 95
QY 134 ---VSNYILSPR-YLGNSPYDIALVKLSAPVYTKHQIPICLOASTFEFENETDCWVTGW 189
DQ 96 LLAIVSRITHTPTFYATQNGADIALLELKNPVNISHHFEVSLPPASETPPSGLTCLWVTGW 155
QY 190 GYKEDALPSHTLOEQVOVAIINNSMCNHLFLKYSFKD---IFGDMVCGNAGGKXD 245
DQ 156 GNIDNDVSLPPFPPLKEVQVPPVENCLDLKHKGVYTGDNHIVRDDMLCAGNE--GHD 213
QY 246 ACPGDSGGPLACNKGMLWQIGVSGVCGGRNRPVGVYTNISHHFEWIK 296
DQ 214 SCQSGSGGLCKVCKVNGTWLQAGVSWGEGCALPNRPGIYTRYTYLDWIHR 264

RESULT 13
TRYT_PIG
ID TRYT_PIG STANDARD; PRT; 275 AA.
AC Q9N2D1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Trypsin precursor (EC 3.4.21.59).
GN MCT7.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=20285343; PubMed=10824103;
RA Chen Y., Shiota M., Ohuchi M., Towatari T., Tashiro J., Murakami M.,
RA Yano M., Yang B., Kido H.;
RT "Mast cell tryptase from pig lungs triggers infection by pneumotropic
RT Sendai and influenza A-viruses. Purification and characterization.";
RL Eur. J. Biochem. 267:3189-3197(2000).
CC -!- FUNCTION: Trypsin is the major neutral protease present in mast
CC cells and is secreted upon the coupled activation-degranulation
CC response of this cell type.

```


CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but
 CC with more restricted specificity than trypsin.
 CC -1- SUBUNIT: Homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Released from the secretory granules upon
 CC mast cell activation.
 CC -1- SIMILARITY: Belongs to peptidase family S1. Trypsin subfamily.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AB038652; BAA93614.1; -;
 CC HSP; P20231; IAAO.
 CC MEROPS; S01.143; -;
 CC InterPro; IPR009003; Cys_Ser_trypsin.
 CC InterPro; IPR001254; Peptidase_S1.
 CC InterPro; IPR001314; Peptidase_S1A.
 CC Pfam; PF00089; trypsin; 1.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC SMART; SM00200; TRYPSIN_DOM; 1.
 CC PROSITE; PS00240; TRYPSIN_DOM; 1.
 CC PROSITE; PS00134; TRYPSIN_HIS; 1.
 CC PROSITE; PS00135; TRYPSIN_SER; 1.
 CC Hydrolase; Serine protease; Signal; Glycoprotein; Zymogen.
 CC KW Hydrolyase; Serine protease; Signal; Glycoprotein; Zymogen.
 CC FT SIGNAL 1 20 POTENTIAL.
 CC FT PROPEP 21 30 ACTIVATION PEPTIDE (BY SIMILARITY).
 CC FT CHAIN 31 275 TRYPTASE.
 CC FT ACT_SITE 74 74 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC FT ACT_SITE 121 121 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC FT ACT_SITE 224 224 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC FT DISULFID 59 75 BY SIMILARITY.
 CC FT DISULFID 155 230 BY SIMILARITY.
 CC FT DISULFID 188 211 BY SIMILARITY.
 CC FT DISULFID 220 248 BY SIMILARITY.
 CC FT CARBOHYD 132 132 N-LINKED (GLCNAC. .) (POTENTIAL).
 CC FT CARBOHYD 233 233 N-LINKED (GLCNAC. .) (POTENTIAL).
 CC SQ SEQUENCE 275 AA; 30439 MW; ACC582647FCCB973 CRC64;
 CC -----
 CC Query Match 29.1%; Score 522; DB 1; Length 275;
 CC Best Local Similarity 42.7%; Pred. No. 1.6e-39;
 CC Matches 114; Conservative 34; Mismatches 93; Indels 26; Gaps 9;
 CC -----
 CC QY 40 APLSGCGRVITSRVGGDEALGRWPQGSRLWD---SHVGVSLSHRWALTAHC 96
 CC DB 19 APAPGQALER---AGIVGKREAPCHKWPQVSLRCLDQYWKHFCGSLHPQWLTAHC 75
 CC QY 97 FEIYSDLSDFSGWMVQFGLTSPFWSLQAVY--TRYFVSNLYLSRVLGN-SPYDIAL 153
 CC DB 76 FG--PEKADPLYTRVQLGE-----QHLYIQDRLLVLSRVLVHPNTYDEVNGADIAL 124
 CC QY 154 VKLSAPVYTKHIQICLQASTFEFNRTDCWVTGWGTYKDEALPSHTLOEVOVAITN 213
 CC DB 125 LELEDPNVLSHSHVQVTLPPASETFPKTRCWTGWGVHSGWFLPPYPLQVRVPIVE 184
 CC QY 214 NSMCN---HLFLKYSFRKDF-CDMVCAGNAQGGKACDGDGGPLACHNGWLWQIGVV 269
 CC DB 185 NSCEDMWOYHGLSTGNIPIVRDMLCAGSE--GHDSCQDGGGGLVCRVNGTWLQAGVV 242
 CC QY 270 SWGVGGRPNRPGVYTNISHFEWIK 296
 CC DB 243 SWEGGALPNRPGIYTRVTHYLDWIHQ 269
 CC -----
 CC RESULT 14
 CC BSS4 MOUSE STANDARD; PRT; 306 AA.
 CC ID BSS4 MOUSE
 CC AC QSER10;
 CC DT 16-OCT-2001 (Rel. 40, Created)
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Brain-specific serine protease 4 precursor (EC 3.4.21.-) (BSSP-4).
 GN PRS22 OR PRS26 OR BSSP4.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC TISSUE=Brain;
 CC RC
 CC RA Mitsui S., Okui A., Kominami K., Yamaguchi N.;
 CC "Cloning and characterization of a novel serine protease, mBSSP-4";
 CC Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to peptidase family S1.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AB010778; BAB20262.1; -;
 CC HSP; P00763; IDPO.
 CC MEROPS; S01.252; -;
 CC MGD; MGI:1918085; 4733401N09Rik.
 CC InterPro; IPR009003; Cys_Ser_trypsin.
 CC InterPro; IPR001254; Peptidase_S1.
 CC InterPro; IPR001314; Peptidase_S1A.
 CC Pfam; PF00089; trypsin; 1.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC SMART; SM00200; TRYPSIN_DOM; 1.
 CC PROSITE; PS00240; TRYPSIN_DOM; 1.
 CC PROSITE; PS00134; TRYPSIN_HIS; 1.
 CC PROSITE; PS00135; TRYPSIN_SER; 1.
 CC Hydrolase; Serine protease; Signal.
 CC FT SIGNAL 1 32 POTENTIAL.
 CC FT CHAIN 33 306 BRAIN-SPECIFIC SERINE PROTEASE 4.
 CC FT ACT_SITE 90 90 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC FT ACT_SITE 141 141 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC FT ACT_SITE 242 242 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC FT DISULFID 75 91 BY SIMILARITY.
 CC FT DISULFID 175 248 BY SIMILARITY.
 CC FT DISULFID 208 227 BY SIMILARITY.
 CC FT DISULFID 238 266 BY SIMILARITY.
 CC FT CARBOHYD 70 70 N-LINKED (GLCNAC. .) (POTENTIAL).
 CC SQ SEQUENCE 306 AA; 33262 MW; FBBF03C0C285E7E8 CRC64;
 CC -----
 CC Query Match 29.0%; Score 520; DB 1; Length 306;
 CC Best Local Similarity 38.0%; Pred. No. 2.8e-39;
 CC Matches 113; Conservative 54; Mismatches 102; Indels 28; Gaps 7;
 CC -----
 CC QY 20 LLLALLARAGLRKPSQEAAPLSGPGRRVITSRVGGDEALGRWPQGSRLWDVSHV 79
 CC DB 19 ILLVLLSTA---PISAATIRVPCGKQQLNRIVGGSDMDAQWPWIVSLKNGSHH 74
 CC QY 80 CGVSLSHRWALTAHCFTETYSYDLSGPGWMVQFGLTSPFWSLQAVYTR---YFVSN 136
 CC DB 75 CAGSLINRWVWVTAACHFK--SNMDKPSLSFVLGA-----WKLSPGPRSQKVGIAW 125
 CC QY 137 IYLSPRY--LQNSPYDIALVKLSAPVYTKHIQICLQASTFEFNRTDCWVTGWGTYKE 194
 CC DB 126 VLPHPRYSWKEGTHADIALVRLHSIQFSRILPICLPDSSVRLPPKTDQWIAWGSIQD 185
 CC QY 195 DEALPSHTLOEVOVAITNNSMCNHLFLKYSFRKDFGDMVCAGNAQGGKACDGDGGP 254
 CC DB 186 GVPLPFQTLQKLVPIIDSELCKSLYRWGAGGAEITEGMLCAGYLEGERDACLGGSGGP 245
 CC QY 255 LACNKGWLWQIGVWVGCGRPNRPGVYTNISHFEWIK 302
 CC DB 246 LMCQVDDHMLLTGIISWEGCA--DDREGVYTSLLAHSRVTQIRIVQGVQLRGLADSG 301

```

RESULT 15
TRBL_HUMAN
ID Q15661; Q15663; Q9H2Y4; PRT; 275 AA.
AC Q15661; Q15663; Q9H2Y4;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Trypsin beta-1 precursor (EC 3.4.21.59) (Trypsin 1) (Trypsin II).
GN TP5B1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=90251647; PubMed=2187193;
RA Vanderslice P., Ballinger S.M., Tam E.K., Goldstein S.M., Craik C.S.,
RA Caughey G.H.;
RT "Human mast cell tryptase: multiple cDNAs and genes reveal a multigene
RT serine protease family";
RL Proc. Natl. Acad. Sci. U.S.A. 87:3811-3815(1990).
[2]
RN SEQUENCE FROM N.A.
RX MEDLINE=9921069; PubMed=9920877;
RA Pallao M., Fejzo M.S., Shayesteh L., Blount J.L., Caughey G.H.;
RA Hettiaratchi A., King G., Heywood G.J., Huang C., Stevens R.L.,
RA Hunt J.E.;
RT "Molecular cloning and characterization of novel human tryptase cDNAs
RT and solving variants.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Trypsin is the major neutral protease present in mast
CC cells and is secreted upon the coupled activation-degranulation
CC response of this cell type.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but
CC with more restricted specificity than trypsin.
CC -!- SUBUNIT: Homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Released from the secretory granules upon
CC mast cell activation.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q15661-1; Sequence=displayed;
CC Name=2;
CC IsoId=Q15661-2; Sequence=VSP_005375;
CC -!- SIMILARITY: Belongs to peptidase family S1. Trypsin subfamily.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M33494; AAC83172.1; -
CC EMBL; M33491; AAA36778.1; -
CC EMBL; AF099144; RAD17860.1; -
CC EMBL; AF206667; AAC35697.1; -
CC PIR; A35863; A35863.
CC HSP; P20231; 1A0L.
CC MEROPS; S01.242; -
CC Genew; HGNC:12019; TP5B1.
CC MIM; 191081; -
CC InterPro; IPR009003; Cys_Ser_trypsin.
CC InterPro; IPR001254; Peptidase_S1.
CC InterPro; IPR001314; Peptidase_S1A.

```

```

Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PROSITE; PS02440; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; signal; Glycoprotein; Zymogen;
KW Alternative splicing; Polymorphism.
FT SIGNAL 1 18 POTENTIAL.
FT PROPEP 19 30 ACTIVATION PEPTIDE (BY SIMILARITY).
FT CHAIN 31 275 TRYPTASE BETA-1.
FT ACT_SITE 74 74 CHARGE RELAY SYSTEM.
FT ACT_SITE 121 121 CHARGE RELAY SYSTEM.
FT ACT_SITE 224 224 CHARGE RELAY SYSTEM.
FT DISULFID 59 75 BY SIMILARITY.
FT DISULFID 155 230 BY SIMILARITY.
FT DISULFID 188 211 BY SIMILARITY.
FT DISULFID 220 248 BY SIMILARITY.
FT CARBOHYD 132 132 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 233 233 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPIC 79 87 Missing (in isoform 2).
FT VARIANT 18 18 /FTID=VSP_005375.
FT VARIANT 23 23 A -> V (in dbSNP:1800984).
FT VARIANT 23 23 /FTID=VAR_014557.
FT VARIANT 85 85 G -> V (in dbSNP:1800986).
FT VARIANT 132 132 A -> T (in dbSNP:2234902).
FT VARIANT 132 132 /FTID=VAR_014559.
FT VARIANT 141 141 N -> K (in dbSNP:1800991).
FT VARIANT 141 141 T -> A (in dbSNP:1800992).
FT VARIANT 162 162 /FTID=VAR_014560.
FT VARIANT 170 170 D -> N (in dbSNP:2234641).
FT VARIANT 170 170 P -> S (in dbSNP:2234904).
FT VARIANT 215 215 /FTID=VAR_014562.
FT VARIANT 216 216 T -> S (in dbSNP:2234905).
FT VARIANT 216 216 R -> Q (in dbSNP:2234906).
FT SEQUENCE 275 AA; 30515 MW; ADC48FDC51F37112 CRC64;
Query Match 28.7%; Score 515; DB 1; Length 275;
Best Local Similarity 40.3%; Pred. No. 6.9e-39;
Matches 116; Conservative 42; Mismatches 92; Indels 38; Gaps 11;
QY 20 LLLAL--LLRAGLRKPKESQEAAPLSGCGRRVITSRVGGEDAEELGRWPHQGSRL--- 74
Db 5 LLLALPVLASRA-----YAAPAQALQVR---GIVGQEAAPRKRPWQVSLRVHGP 53
QY 75 -WDGHVCGVSLLSHRWALTAHCFETYSDLSDPSGMWVQGLTSMPSFWSLQAYTRYF 133
Db 54 YW-NHFQGGSLHPQWVLTAAHC--VGPDKVLAALRVQLRE-----QHLVYQDL 101
QY 134 --VSNIVLSRP-VLGNSPYDIALVKLSAPVYTHYHQIPIQLQASTFEFEFRDCTWGTWG 190
Db 102 LPVSRIRVHPQFYTAQIGADIALLELEEPVNVSSHVHTVTLPPASSETFPFGMPQWVTWG 161
QY 191 YIKDEALPSPHTLQEVQVAIINNMCNHLFLKYSFKD---IFGDMVCAAGNAQGGKDA 246
Db 162 DVDNDRLLPFPPLKQVKVPIMENHICDAKVLGAYTGDDVIRVDRDMLCAGNTR--RDS 219
QY 247 CFGDSGGFLACNKNGLWYQGVVSWGVGCGRRPDRPGVYTNISHHFEWI 294
Db 220 CQDGGGGLVCKVNGTGLQAGVSWGEGCAQPNRPRTYTRVYLDWI 267

```

Search completed: April 6, 2004, 14:12:06
Job time : 18 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2004, 14:05:19 ; Search time 59 Seconds
(without alignments)
1565.984 Million cell updates/sec

Title: US-09-787-844-2

Perfect score: 1792

Sequence: 1 RRGQGAAGEAMGARGAL.....PSWPLLFPLLWALPLGPV 327

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1792	100.0	327	3 AAY91871	Human can
2	1728	96.4	314	2 AAU77296	Amino aci
3	1728	96.4	314	2 AAU97116	A human e
4	1728	96.4	314	2 AAU06434	Human pro
5	1728	96.4	314	2 AAY13388	Amino aci
6	1728	96.4	314	3 AAB12132	Hydrophob
7	1728	96.4	314	3 ADC78569	Human PRO
8	1728	96.4	314	4 AAB80256	Human PRO
9	1728	96.4	314	4 AAU02223	Human ext
10	1728	96.4	314	5 AAE17010	Human eos
11	1728	96.4	314	6 ABU71634	Human PRO
12	1728	96.4	314	6 ABU71489	Human PRO
13	1728	96.4	314	6 ABU71935	Human sec
14	1728	96.4	314	6 ABO01818	Novel hum
15	1728	96.4	314	6 ABO01818	Human sec
16	1728	96.4	314	6 ABO04706	Human sec
17	1728	96.4	314	6 ABU64543	Human sec
18	1728	96.4	314	6 ABU67389	Human sec
19	1728	96.4	314	6 ABO14909	Human sec
20	1728	96.4	314	6 ABU69666	Novel hum
21	1728	96.4	314	6 ABO14848	Human sec
22	1728	96.4	314	6 ADB29462	Human sec
23	1728	96.4	314	6 ADA18181	Human sec
24	1728	96.4	314	6 ABO32800	Human sec
25	1728	96.4	314	6 ABO34860	Human PRO

26	1728	96.4	314	6 ADA16293	Human sec
27	1728	96.4	314	6 ADA42438	Human sec
28	1728	96.4	314	6 ABO17538	Human PRO
29	1728	96.4	314	7 ADA16717	Human sec
30	1728	96.4	314	7 ADA13146	Human sec
31	1728	96.4	314	7 ADA42014	Human sec
32	1728	96.4	314	7 ADA17361	Human sec
33	1728	96.4	314	7 ADA42864	Human sec
34	1728	96.4	314	7 ABO17599	Human PRO
35	1728	96.4	314	7 ADB80572	Ovarian c
36	1728	96.4	314	7 ADB77783	Human sec
37	1728	96.4	314	7 ADB74919	Human sec
38	1728	96.4	314	7 ADC28565	Human sec
39	1728	96.4	314	7 ADC39765	Human sec
40	1728	96.4	314	7 ADC40279	Human sec
41	1728	96.4	314	7 ADC19103	Human sec
42	1728	96.4	314	7 ADC34403	Human sec
43	1728	96.4	314	7 ADC29458	Human sec
44	1728	96.4	314	7 ADC38989	Human sec
45	1728	96.4	314	7 ADC40874	Human sec

ALIGNMENTS

RESULT 1

AY91871

ID AY91871 standard; protein; 327 AA.

XX AC AY91871;

DT 19-JUL-2000 (first entry)

DE Human cancer-specific gene protein, Pro104.

XX Human cancer-specific gene protein; Pro104; serine protease; diagnosis;

XX staging; imaging; treating; gynecologic cancer; testicular cancer.

XX Homo sapiens.

OS Homo sapiens.

PH Key

FT Domain

FT Location/Qualifiers

FT 54..58

FT /note= "conserved serine protease motif"

FT Cleavage-site

FT 54..55

FT Domain

FT 55..327

FT /label= active_protease_domain

XX XX

XX WC200016805-A1.

XX PD 30-MAR-2000.

XX PF 23-SEP-1999; 99WO-US021774.

XX PR 23-SEP-1998; 98US-0101522P.

XX PA (DIAD-) DIADEXUS LLC.

XX PI Ali SM, Caferkey R;

XX WPI; 2000-283453/24.

XX DR N-PSDB; AAA08505.

XX PT Methods for diagnosing, staging, imaging and treating gynecologic and

XX testicular cancers by measuring expression of a cancer specific gene.

XX Example 2; Page 32-33; 36pp; English.

XX This protein sequence is encoded by human cancer-specific gene (CSG),

XX Pro104. Pro104 is a serine protease that shares 31 percent homology with

XX human hepsin at the amino acid level. When aligned with other serine

XX proteases, Pro104 shares all the conserved amino acid motifs that are

XX characteristic of all other serine proteases, in particular a highly

XX conserved RIVGG sequence (see AAY91872). The inventive methods comprise

CC measuring expression of CSG in order to diagnose, stage, image and treat
 CC gynecologic and testicular cancers. The levels of CSG are compared to
 CC levels found in a normal human control (a change in the measured level of
 CC CSG is associated with the presence of the cancer). The early diagnosis
 CC of cancers improves the success rate of therapeutic protocols
 XX
 SQ Sequence 327 AA;

Query Match 100.0%; Score 1792; DB 3; Length 327;
 Best Local Similarity 100.0%; Pred. NO. 9.8e-154;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RRQRGAAGEEANGARGALLALLARAGLRKPESQEAAPLSGPCRRVITSRIYGGED 60
 DB 1 RRQRGAAGEEANGARGALLALLARAGLRKPESQEAAPLSGPCRRVITSRIYGGED 60
 QY 61 AELGRWQOGLRLWDSHVCVLSLHSHRWALTAHCFETYSDSLSDSGMWVQFQJLTSMP 120
 DB 61 AELGRWQOGLRLWDSHVCVLSLHSHRWALTAHCFETYSDSLSDSGMWVQFQJLTSMP 120
 QY 121 SFMSLOAYTRYFYVSNLYLSPRYLNSPYDIALVKLSAPVYTKHQICLOASTFEFEN 180
 DB 121 SFMSLOAYTRYFYVSNLYLSPRYLNSPYDIALVKLSAPVYTKHQICLOASTFEFEN 180
 QY 181 RTDCWVTGWYIKEDEALPSHTLOEVQVVAIIINNSMNCNHLFLKYSRDKDIFGDMVCAGNA 240
 DB 181 RTDCWVTGWYIKEDEALPSHTLOEVQVVAIIINNSMNCNHLFLKYSRDKDIFGDMVCAGNA 240
 QY 241 QGGKDCACFGDSGGPLACNKNGLWYQGVSWGVCGRPNRPBGVYTNISHHFEWIOKMAQ 300
 DB 241 QGGKDCACFGDSGGPLACNKNGLWYQGVSWGVCGRPNRPBGVYTNISHHFEWIOKMAQ 300
 QY 301 SGMSQDPDPWPLFFPPLLWALPLGPV 327
 DB 301 SGMSQDPDPWPLFFPPLLWALPLGPV 327

RESULT 2
 AAW77296
 ID AAW77296 standard; protein; 314 AA.

AC AAW77296;
 XX 07-JAN-1999 (first entry)
 DE Amino acid sequence of the short isoform of HELA2.
 XX Serine protease; regulation; cell activity; viability; HELA2; ATC2;
 KW BCOM3; testis; fertility; suppressor; testicular germ cell cancer;
 KW seminoma; testis-specific expression; antitumour; sperm development;
 XX infertility.

OS Homo sapiens.
 XX WO9836054-A1.
 DN 20-AUG-1998.
 XX 13-FEB-1998; 98WO-AU000085.
 XX 13-FEB-1997; 97AU-00005101.
 PR 18-NOV-1997; 97AU-00000422.
 XX (AMRA-) AMRAD OPERATIONS PTY LTD.
 XX Antalis TM, Hooper JD;
 PI WPI; 1998-480768/41.
 DR N-PSDB; AAV59118.

XX New serine protease(s) and kinase involved in regulating cell activity
 PT and viability - particularly the testis-specific protease HELA2 used for
 PT modulation of fertility and as tumour suppressor.

XX

Claim 2; Fig 6; 167pp; English.

XX The present sequence represents the amino acid sequence of the short
 CC isoform of HELA2. cDNA generated from HeLa cells and PAI-2 expressing
 CC HeLa cells was amplified using PCR primers AAV48312-13. Three new
 CC sequences were detected in the 480 bp amplicon. These sequences are
 CC designated HELA2 and ATC2 which have high homology to serine proteases
 CC and BCOM3 which has homology to a kinase. The proteins are involved in or
 CC associated with regulation of cell activity and/or viability.
 CC Administration of recombinant HELA2 (also called testisin) is used to
 CC increase fertility. Downregulation of HELA2 reduces fertility. HELA2 is
 CC also a suppressor of testicular germ cell cancers (seminoma) and is also
 CC expressed in some non-testicular cancers (of colon, pancreas, prostate
 CC and ovary), so is a marker/potential therapeutic target for cancer. The
 CC promoter from the HELA2 gene is useful for testis-specific expression of
 CC other genes, e.g. for gene therapy or modulation of fertility. Drugs that
 CC block activity of HELA2 should have antitumour activity (other than in
 CC testis) while in testis recombinant HELA2 should stop growth of tumours
 CC and normalise sperm development (eliminating the need for orchidectomy).
 CC Identification of mutant forms of HELA2 can be used to diagnose
 CC infertility

SQ Sequence 314 AA;

Query Match 95.4%; Score 1728; DB 2; Length 314;
 Best Local Similarity 100.0%; Pred. NO. 5.8e-148;
 Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 14 MGARGALLALLARAGLRKPESQEAAPLSGPCRRVITSRIYGGEDAEGLRWPQGSRLR 73
 DB 1 MGARGALLALLARAGLRKPESQEAAPLSGPCRRVITSRIYGGEDAEGLRWPQGSRLR 60
 QY 74 LWDSHVCVLSLHSHRWALTAHCFETYSDSLSDSGMWVQFQJLTSMPFSLQAYTRYF 133
 DB 61 LWDSHVCVLSLHSHRWALTAHCFETYSDSLSDSGMWVQFQJLTSMPFSLQAYTRYF 120
 QY 134 VSNLYLSPRYLNSPYDIALVKLSAPVYTKHQICLOASTFEFENRTDCWVTGWYIK 193
 DB 121 VSNLYLSPRYLNSPYDIALVKLSAPVYTKHQICLOASTFEFENRTDCWVTGWYIK 180
 QY 194 EDEALPSHTLOEVQVVAIIINNSMNCNHLFLKYSRDKDIFGDMVCAGNAQGGKDCACFGDSGG 253
 DB 181 EDEALPSHTLOEVQVVAIIINNSMNCNHLFLKYSRDKDIFGDMVCAGNAQGGKDCACFGDSGG 240
 QY 254 PLACNKNGLWYQGVSWGVCGRPNRPBGVYTNISHHFEWIOKMAQSGMSQDPDPWPL 313
 DB 241 PLACNKNGLWYQGVSWGVCGRPNRPBGVYTNISHHFEWIOKMAQSGMSQDPDPWPL 300
 QY 314 FFPPLLWALPLGPV 327
 DB 301 FFPPLLWALPLGPV 314

RESULT 3

AAW97116
 ID AAW97116 standard; protein; 314 AA.

AC AAW97116;

XX 04-MAY-1999 (first entry)

DE A human eosinophil serine protease.

XX Human; eosinophil; serine protease; allergic disease; infectious disease;
 KW tumour; granulomatous disease; collagen disease; vascular inflammation.

OS Homo sapiens.

XX JPI1032768-A.

XX 09-FEB-1999.

XX

```

PF 16-JUL-1997; 97JP-00191319.
XX
PR 16-JUL-1997; 97JP-00191319.
XX
PA (ONOF) ONO PHARM CO LTD.
XX
DR WPI; 1999-183825/16.
DR N-PSDB; AAX15336.
XX
XX New eosinophils serine protease - useful for prevention and treatment of
PT allergic, infectious, tumor, granulomatous and collagen diseases.
XX
PS Claim 1; Page 9-10; 18pp; Japanese.
XX
XX The present sequence represents a human eosinophil serine protease. The
CC protease is useful in drug compositions for the prevention and treatment
CC of allergic diseases, infectious diseases, tumour diseases, granulomatous
CC diseases, collagen diseases and vascular inflammation
XX
SQ Sequence 314 AA;
Query Match 96.4%; Score 1728; DB 2; Length 314;
Best Local Similarity 100.0%; Pred. No. 5.8e-148;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 MGARGALLALLARAGLRKPESQEAAPLSGCGRRVITSRIVGGEDAEELGRWPQGSRLR 73
Db 1 MGARGALLALLARAGLRKPESQEAAPLSGCGRRVITSRIVGGEDAEELGRWPQGSRLR 60
QY 74 LWDSHVCGVSLSHRWALTAACHCFETYSDLPSCGMVQFGOLTSMPSFWSLQAYTYTF 133
Db 61 LWDSHVCGVSLSHRWALTAACHCFETYSDLPSCGMVQFGOLTSMPSFWSLQAYTYTF 120
QY 134 VSNIVLSRYLGNISPYDIALVKLSAPVYTKHIQICLQASTFEFENRTDCWVTGWGIK 193
Db 121 VSNIVLSRYLGNISPYDIALVKLSAPVYTKHIQICLQASTFEFENRTDCWVTGWGIK 180
QY 194 EDEALPSPTLQEVQVVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAGGKDACFGDSGG 253
Db 181 EDEALPSPTLQEVQVVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAGGKDACFGDSGG 240
QY 254 PLACNKGNGLVQIGVSVGCGRPNRGVYTNISHHFEWIKLMAQSGMSQPPSPNPL 313
Db 241 PLACNKGNGLVQIGVSVGCGRPNRGVYTNISHHFEWIKLMAQSGMSQPPSPNPL 300
QY 314 FPELLWALPLLGPV 327
Db 301 FPELLWALPLLGPV 314
RESULT 4
AAY06434
ID AAY06434 standard; protein; 314 AA.
AC AAY06434;
XX
XX 27-SEP-1999 (first entry)
XX Human protease HUPM-3.
XX
XX Protease; human; HUPM-3; cell proliferation; cancer; immune disorder;
KW inflammation; therapy.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1. 19
FT /note= "putative signal peptide"
FT Protein 20. 314
FT /note= "putative mature protein"
FT Modified-site 39
FT /note= "protein kinase C phosphorylation site"
FT Modified-site 58

```

```

FT Modified-site /note= "protein kinase C phosphorylation site"
FT 73 /note= "protein kinase C phosphorylation site"
FT 82
FT Active-site 86
FT Modified-site /note= "casein kinase II phosphorylation site"
FT 127
FT Modified-site /note= "protein kinase C phosphorylation site"
FT 134
FT Modified-site /note= "casein kinase II phosphorylation site"
FT 161
FT Modified-site /note= "casein kinase II phosphorylation site"
FT 167
FT Modified-site /note= "N-glycosylated"
FT 190
FT Modified-site /note= "casein kinase II phosphorylation site"
FT 200
FT Modified-site /note= "N-glycosylated"
FT 212
FT Modified-site /note= "protein kinase C phosphorylation site"
FT 238
FT Active-site 273
FT Modified-site /note= "N-glycosylated"
FT 291
FT Modified-site /note= "casein kinase II phosphorylation site"
FT W09936550-A2.
XX
XX 22-JUL-1999.
XX
XX 12-JAN-1999; 99MO-US000655.
XX
XX 16-JAN-1998; 98US-00008271.
XX (INCY-) INCYTE PHARM INC.
XX
XX Bandman O, Hillman JL, Yue H, Guegler KJ, Corley NC, Tang YT;
PI Shah P;
XX
XX WPI; 1999-430616/36.
XX N-PSDB; AAX87151.
XX
XX Novel human protease molecules useful in the treatment of developmental
PT disorders and/or cancers.
XX
XX Claim 1; Page 71-72; 90pp; English.
XX
XX The present sequence represents novel human protease HUPM-3, as deduced
CC from the consensus sequence (see AAX87151) of overlapping cDNA clones
CC obtained from various libraries. Northern analysis shows expression of
CC HUPM-3 in cardiovascular, haematopoietic and male reproductive cDNA
CC libraries. Approximately 86% of these libraries are associated with
CC neoplastic disorders. The invention provides 12 new human proteases, i.e.
CC HUPM-1 to -12 (see AAY06432-43), and the polynucleotides encoding them
CC (see AAX87149-60). Also provided are vectors, host cells and methods for
CC producing HUPM polypeptides, as well as agonists and antagonists of HUPM.
CC Methods for treating or preventing cell proliferative disorders and
CC immune disorders using HUPM or HUPM antagonists are claimed
XX
XX Sequence 314 AA;
Query Match 96.4%; Score 1728; DB 2; Length 314;
Best Local Similarity 100.0%; Pred. No. 5.8e-148;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 MGARGALLALLARAGLRKPESQEAAPLSGCGRRVITSRIVGGEDAEELGRWPQGSRLR 73
Db 1 MGARGALLALLARAGLRKPESQEAAPLSGCGRRVITSRIVGGEDAEELGRWPQGSRLR 60
QY 74 LWDSHVCGVSLSHRWALTAACHCFETYSDLPSCGMVQFGOLTSMPSFWSLQAYTYTF 133
Db 61 LWDSHVCGVSLSHRWALTAACHCFETYSDLPSCGMVQFGOLTSMPSFWSLQAYTYTF 120

```

QY 134 VSNYLSPRYLGNRPYDIALVKLSAPVTYTHIQIPICLOASTFEFENRTDCWVTGWGK 193
 Db 121 VSNYLSPRYLGNRPYDIALVKLSAPVTYTHIQIPICLOASTFEFENRTDCWVTGWGK 180
 QY 194 EDEALPSHTLQEVQVAILNNSMCNHLFLKYSFRKDFGDMVCAGNAGGKACFGDSGG 253
 Db 181 EDEALPSHTLQEVQVAILNNSMCNHLFLKYSFRKDFGDMVCAGNAGGKACFGDSGG 240
 QY 254 PLACNKGWLWQIGVWSGVGCGRPNGPVYTNISHFEWIKLMAQSGMSQDPDPSWPLL 313
 Db 241 PLACNKGWLWQIGVWSGVGCGRPNGPVYTNISHFEWIKLMAQSGMSQDPDPSWPLL 300
 QY 314 FFLLLWALPLPGPV 327
 Db 301 FFLLLWALPLPGPV 314

RESULT 5
 AAY13388
 ID AAY13388 standard; protein; 314 AA.
 XX
 AC AAY13388;
 XX
 DT 25-JUN-1999 (first entry)
 XX
 DE Amino acid sequence of protein PRO303.
 XX
 KW Secreted protein; transmembrane protein; human; enterocolitis;
 KW Zollinger-Ellison syndrome; gastrointestinal ulceration;
 KW congenital microvillus atrophy; skin disease; cell growth;
 KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
 KW Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin;
 KW dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic;
 KW wound healing; tissue repair.
 XX
 OS Homo sapiens.
 XX
 EN WO9914328-A2.
 XX
 PD 25-MAR-1999.
 XX
 FF 16-SEP-1998; 98WO-US019330.
 XX
 PR 17-SEP-1997; 97US-0059113P.
 PR 17-SEP-1997; 97US-0059115P.
 PR 17-SEP-1997; 97US-0059117P.
 PR 17-SEP-1997; 97US-0059119P.
 PR 17-SEP-1997; 97US-0059121P.
 PR 17-SEP-1997; 97US-0059122P.
 PR 17-SEP-1997; 97US-0059124P.
 PR 18-SEP-1997; 97US-0059263P.
 PR 18-SEP-1997; 97US-0059266P.
 PR 15-OCT-1997; 97US-0062125P.
 PR 17-OCT-1997; 97US-0062285P.
 PR 17-OCT-1997; 97US-0062287P.
 PR 21-OCT-1997; 97US-0063486P.
 PR 24-OCT-1997; 97US-0062814P.
 PR 24-OCT-1997; 97US-0062816P.
 PR 24-OCT-1997; 97US-0063045P.
 PR 24-OCT-1997; 97US-0063120P.
 PR 24-OCT-1997; 97US-0063121P.
 PR 24-OCT-1997; 97US-0063127P.
 PR 24-OCT-1997; 97US-0063128P.
 PR 27-OCT-1997; 97US-0063327P.
 PR 27-OCT-1997; 97US-0063329P.
 PR 28-OCT-1997; 97US-0063541P.
 PR 28-OCT-1997; 97US-0063542P.
 PR 28-OCT-1997; 97US-0063544P.
 PR 28-OCT-1997; 97US-0063549P.
 PR 28-OCT-1997; 97US-0063550P.
 PR 28-OCT-1997; 97US-0063564P.
 PR 28-OCT-1997; 97US-0063435P.
 PR 29-OCT-1997; 97US-0063704P.

29-OCT-1997; 97US-0063732P.
 29-OCT-1997; 97US-0063734P.
 29-OCT-1997; 97US-0063735P.
 29-OCT-1997; 97US-0063738P.
 29-OCT-1997; 97US-0064215P.
 31-OCT-1997; 97US-0063870P.
 31-OCT-1997; 97US-0064103P.
 03-NOV-1997; 97US-0064248P.
 07-NOV-1997; 97US-0064809P.
 12-NOV-1997; 97US-0065186P.
 17-NOV-1997; 97US-0065848P.
 18-NOV-1997; 97US-0065693P.
 21-NOV-1997; 97US-0066120P.
 21-NOV-1997; 97US-0066364P.
 24-NOV-1997; 97US-0066453P.
 24-NOV-1997; 97US-0066466P.
 24-NOV-1997; 97US-0066511P.
 24-NOV-1997; 97US-0066770P.
 24-NOV-1997; 97US-0066772P.
 25-NOV-1997; 97US-0066840P.

(GETH) GENENTECH INC.
 Wood WI, Gurney AL, Goddard A, Pennica D, Chen J, Yuan J;
 WPI: 1999-229533/19.
 N-PSDB; AX52259.
 New isolated human genes and polypeptides used in, e.g. treatment of
 gastrointestinal ulceration.
 Claim 12; Fig 92; 320pp; English.
 AAY13344-403 represent secreted and transmembrane human proteins. The
 CDNA sequences are obtained from cDNA libraries, prepared from fetal
 lung, fetal kidney, fetal brain, fetal liver and fetal retina. The
 encoded polypeptides have specific uses based on their homology to known
 polypeptides, e.g. PRO211 and PRO217 can be used for disorders associated
 with the preservation and maintenance of gastrointestinal mucosa and the
 repair of acute and chronic mucosal lesions (e.g. enterocolitis,
 Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital
 microvillus atrophy), skin diseases associated with abnormal keratinocyte
 differentiation (e.g. psoriasis, epithelial cancers such as lung squamous
 cell carcinoma of the vulva and gliomas), potent effects on cell growth
 and development, diseases related to growth or survival of nerve cells
 including Parkinson's disease, Alzheimer's disease, ALS, neuropathies or
 cancer. PRO245 can be used as for fibromodulin, e.g. for reducing dermal
 scarring. PRO264 can be used as a target for anti-tumor drugs. PRO533 may
 be used in the treatment of Usher Syndrome or Atrophia areata; PRO269 can
 be used as an anti-thrombotic agent; PRO287 polypeptides and portions may
 have therapeutic applications in wound healing and tissue repair; PRO317
 can be used for treating problems of the kidney, uterus, endometrium,
 blood vessels, or related tissue, e.g. in the heart of genital tract

Query Match 96.4%; Score 1726; DB 2; Length 314;
 Best Local Similarity 100.0%; Pred. NO. 5.8e-148;
 Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 14 MGARGALLALLARAGLRKPEQAEAPLSPGCGRRVITSRIVGGEDAEIGRHPWQSLR 73
 Db 1 MGARGALLALLARAGLRKPEQAEAPLSPGCGRRVITSRIVGGEDAEIGRHPWQSLR 60
 QY 74 LWDSHVCGVSLLSHRWALTAARHCFTETYSIDLSDPSGMMVQFGLTSMPSFSLQAYTRYF 133
 Db 61 LWDSHVCGVSLLSHRWALTAARHCFTETYSIDLSDPSGMMVQFGLTSMPSFSLQAYTRYF 120
 QY 134 VSNYLSPRYLGNRPYDIALVKLSAPVTYTHIQIPICLOASTFEFENRTDCWVTGWGK 193
 Db 121 VSNYLSPRYLGNRPYDIALVKLSAPVTYTHIQIPICLOASTFEFENRTDCWVTGWGK 180
 QY 194 EDEALPSHTLQEVQVAILNNSMCNHLFLKYSFRKDFGDMVCAGNAGGKACFGDSGG 253

Db 181 EDEALPSPHTLQEVQVAIINNSMNCNHLFLKYSFRKDI FGDWVCAGNAQGGKDACFDGSGG 240
 QY 254 PLACNKNGLWYQIGVSWGVGCGRPNRPVYTNISHHFEWIKLMAQSGMSQDPDSWPLL 313
 Db 241 PLACNKNGLWYQIGVSWGVGCGRPNRPVYTNISHHFEWIKLMAQSGMSQDPDSWPLL 300
 QY 314 FFPILLWALPLLGPV 327
 Db 301 FFPILLWALPLLGPV 314

RESULT 6
 AAB12132
 ID AAB12132 standard; protein; 314 AA.
 XX
 AC AAB12132;
 XX
 DT 02-FEB-2001 (first entry)
 DE
 XX Hydrophobic domain protein from clone HP03116 isolated from KB cells.
 XX
 KW Human; secreted protein; membrane protein; hydrophobic domain;
 KW proliferation control; differentiation induction; material transport;
 KW biophylaxis; signal receptor; ion channel; transporter; immunostimulant;
 KW immunosuppressant; haematopoiesis regulator; chemotactic; chemokinetic;
 KW haemostatic; thrombolytic; anti-inflammatory; tumour inhibition;
 KW autoimmune disease; Alzheimer's disease; Parkinson's disease; cancer.
 XX
 OS Homo sapiens.
 XX
 XX
 XX W0200028448-A2.
 XX
 XX 25-MAY-2000.
 XX
 XX 17-NOV-1999; 99WO-JP006412.
 XX
 XX 17-NOV-1998; 98JP-00326255.
 XX
 XX 22-DEC-1998; 98JP-00364315.
 XX
 XX 16-MAR-1999; 99JP-00069811.
 XX
 XX 27-APR-1999; 99JP-00119299.
 XX
 XX 19-MAY-1999; 99JP-00138169.
 XX
 XX (SAGA) SAGAMI CHEM RES CENT.
 XX
 XX (PROT-) PROTEGENE INC.
 XX
 XX Kato S, Kimura T;
 XX
 XX WPI; 2000-387753/33.
 XX
 XX N-PSDB; AAA62005, AAA62015.
 XX
 XX Proteins comprising hydrophobic regions, such as secretory and membrane
 PT proteins, useful in research and diagnostics and having various
 PT activities e.g. immunomodulatory, anti-inflammatory, chemokinetic,
 XX hemostatic, thrombolytic.
 XX
 XX Claim 1; Page 238-240; 410pp; English.
 XX
 XX
 CC Secretory proteins play important roles in the proliferation control, the
 CC differentiation induction, the material transport and the biophylaxis of
 CC cells. Membrane proteins have important roles as signal receptors, ion
 CC channels and transporters. The present sequence is a human protein which
 CC has at least one hydrophobic domain. This protein may be a secretory or a
 CC membrane protein. The present protein may have cytokine and cell
 CC proliferation/differentiation activity, immune stimulating or suppressing
 CC activity, haematopoiesis activity, tissue growth activity,
 CC activ/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, anti-inflammatory activity and tumour
 CC inhibition activity. The present protein could therefore be used for
 CC treatment of autoimmune disease, Alzheimer's disease, Parkinson's
 CC disease, and cancer
 XX
 XX Sequence 314 AA;

Query Match 96.4%; Score 1728; DB 3; Length 314;
 Best Local Similarity 100.0%; Pred. No. 5.8e-148;
 Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 14 MGARGALLALLARAGLRKPFESQEAAPLSGPCRRVITSRIVGGEDAELGRWPQGSRLR 73
 Db 1 MGARGALLALLARAGLRKPFESQEAAPLSGPCRRVITSRIVGGEDAELGRWPQGSRLR 60
 QY 74 LWDSHVCGVSLLSHRWALTAARCFETYSDSLSDPSGMVQFQGLTSMPSFWSLQAYTYRYF 133
 Db 61 LWDSHVCGVSLLSHRWALTAARCFETYSDSLSDPSGMVQFQGLTSMPSFWSLQAYTYRYF 120
 QY 134 VSNITLSPRYLGNSPYDIALVKLSAPVYTKHIQICLOASTFFENRTDCWVTGWGIK 193
 Db 121 VSNITLSPRYLGNSPYDIALVKLSAPVYTKHIQICLOASTFFENRTDCWVTGWGIK 180
 QY 194 EDEALPSPHTLQEVQVAIINNSMNCNHLFLKYSFRKDI FGDWVCAGNAQGGKDACFDGSGG 253
 Db 181 EDEALPSPHTLQEVQVAIINNSMNCNHLFLKYSFRKDI FGDWVCAGNAQGGKDACFDGSGG 240
 QY 254 PLACNKNGLWYQIGVSWGVGCGRPNRPVYTNISHHFEWIKLMAQSGMSQDPDSWPLL 313
 Db 241 PLACNKNGLWYQIGVSWGVGCGRPNRPVYTNISHHFEWIKLMAQSGMSQDPDSWPLL 300
 QY 314 FFPILLWALPLLGPV 327
 Db 301 FFPILLWALPLLGPV 314

RESULT 7
 ADC78569
 ID ADC78569 standard; protein; 314 AA.
 XX
 AC ADC78569;
 XX
 DT 01-JAN-2004 (first entry)
 DE
 XX Human PRO303 protein.
 XX
 KW antiinflammatory; antiulcer; cytostatic; antipsoriatic; antiparkinsonian;
 KW neurotrophic; neuroprotective; vasotropic; chemotactic; angiogenic;
 KW antiarthritic; osteopathic; antiasthmatic; antiarthritic; antihemetic;
 KW antiarteriosclerotic; cardiast; antidiabetic; cerebroprotective;
 KW thrombolytic; immunomodulator; enterocolitis; Zollinger-Ellison syndrome;
 KW gastrointestinal ulceration; psoriasis; cancer; Parkinson's disease;
 KW Alzheimer's; ALS; neuropathy; dermal scarring; wound healing;
 KW nerve repair; thrombosis; bone; cartilage formation; angiogenesis;
 KW asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disorder;
 KW atherosclerosis; cardiac injury; infertility; premature aging; AIDS;
 XX diabetes; stroke; gene therapy; transgenic; PRO; human.
 XX
 OS Homo sapiens.
 XX
 XX W0200015796-A2.
 XX
 XX 23-MAR-2000.
 XX
 XX 15-SEP-1999; 99WO-US021090.
 XX
 XX 16-SEP-1998; 98WO-US019330.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Chen J, Goddard A, Gurney AL, Hillan K, Pennica D, Wood WI;
 XX Yuan J;
 XX WPI; 2000-271434/23.
 XX
 XX N-PSDB; ADC78568.
 XX
 XX Novel nucleic acids encoding secreted and transmembrane polypeptides with
 PT homology, e.g. to growth and cancer-associated antigens.
 XX

Db 301 FPLLMALPLGPV 314
|||||
RESULT 9
AAU02223
ID AAU02223 standard; protein; 314 AA.
XX
AC AAU02223;
XX
DT 29-AUG-2001 (first entry)
XX
DE Human extracellular serine protease TADG-16.
XX
KW Human; extracellular serine protease; tumour antigen derived gene-16;
KW TADG-16; ovarian carcinoma; breast cancer; lung cancer; colon cancer;
KW prostate cancer; HLA type.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..17
FT /label= Signal_secretion_sequence
FT Protein 18..314
FT /label= Secreted_TADG-16_protein
FT Region 76..83
FT /notes "Region containing His residue of conserved
FT catalytic triad found in serine proteases"
FT Region 137..141
FT /notes "Region containing Asp residue of conserved
FT catalytic triad found in serine proteases"
FT Region 236..241
FT /notes "Region containing Ser residue of conserved
FT catalytic triad found in serine proteases"
XX
WO200127257-A1.
XX
PD 19-APR-2001.
XX
PF 13-OCT-2000; 2000WO-US028558.
XX
PR 14-OCT-1999; 99US-00418527.
XX
PA (UYAR-) UNIV ARKANSAS.
XX
PI O'Brien TJ, Underwood LJ, Shigemasa K;
XX
DR N-PSDB; AA501698.
XX
PS New tumor antigen-derived gene-16 protein, useful for diagnosis and
treatment of ovarian, breast, lung, colon and prostate cancer.
XX
PS Claim 3; Fig 4; 124pp; English.
XX
CC The present sequence represents a novel human extracellular serine
protease, tumour antigen derived gene-16 (TADG-16) protein. TADG-16 is
expressed in normal ovaries and testes and in certain ovarian carcinomas.
TADG-16 contains the conserved catalytic triad, His-Asp-Ser, and a signal
secretion sequence characteristic of the serine protease family. An
antisense oligonucleotide having a complementary sequence to the TADG-16
nucleic acid is useful for treating various cancers, including ovarian,
breast, lung, colon and prostate. The TADG-16 nucleic acid, TADG-16
protein and antibodies specific to TADG-16 are useful for the diagnosis
of cancer. TADG-16 protein or its fragments are useful for vaccinating an
individual against TADG-16. Numerous TADG-16 peptides (AAU02225-AAU02384)
are tested for their binding affinity to the 8 haplotypes HLA A0201, HLA
A0205, HLA A1, HLA A24, HLA B7, HLA B8, HLA B2702, and HLA B403
XX
SQ Sequence 314 AA;
Query Match 96.4%; Score 1728; DB 4; Length 314;
Best Local Similarity 100.0%; Pred. No. 5.8e-148;

Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 14 MGARGALLALLARAGLRKPESEAAAPLSGPGRRVITSRIYGGDAELGRWPGQSLR 73
Db 1 MGARGALLALLARAGLRKPESEAAAPLSGPGRRVITSRIYGGDAELGRWPGQSLR 60
Qy 74 LWDSHVGVSLLSHRWALTAHCFETYSDLSDSPGVMVQGLTSPFSLQAYTRYF 133
Db 61 LWDSHVGVSLLSHRWALTAHCFETYSDLSDSPGVMVQGLTSPFSLQAYTRYF 120
Qy 134 VSNILSPRYLGNSPYDIALVKLSAPVYTKHTQICLQASTFEFFENRTDCWTGWGIK 193
Db 121 VSNILSPRYLGNSPYDIALVKLSAPVYTKHTQICLQASTFEFFENRTDCWTGWGIK 180
Qy 194 EDALSPHPLQEVQVAIINNSMCHLFLKYSFRKDFGDMVCAAGKACFGDSGG 253
Db 181 EDALSPHPLQEVQVAIINNSMCHLFLKYSFRKDFGDMVCAAGKACFGDSGG 240
Qy 254 PLACNKNGLWYQIGVYSGVGGCRRPNRPVYTNISHHFEWIKLMAQSGMSQDPSPWLL 313
Db 241 PLACNKNGLWYQIGVYSGVGGCRRPNRPVYTNISHHFEWIKLMAQSGMSQDPSPWLL 300
Qy 314 FPLLMALPLGPV 327
Db 301 FPLLMALPLGPV 314
RESULT 10
AAE17010
ID AAE17010 standard; protein; 314 AA.
XX
AC AAE17010;
XX
DT 18-APR-2002 (first entry)
XX
DE Human eosinophil serine protease-1 (esp-1) like enzyme #2.
XX
KW Human; eosinophil serine protease-1; esp-1; enzyme; antiinflammatory;
KW antiasthmatic; antiallergic; osteopathic; cytostatic; dermatological;
KW asthma; airway allergy; chronic obstructive pulmonary disease; COPD;
KW osteoporosis; dermatitis; Paget's disease; therapy.
XX
OS Homo sapiens.
XX
PN WO200198503-A2.
XX
PD 27-DEC-2001.
XX
PF 20-JUN-2001; 2001WO-EF006936.
XX
PR 21-JUN-2000; 2000US-0212844P.
PR 31-OCT-2000; 2000US-0244171P.
PR 30-MAR-2001; 2001US-0279766P.
XX
PA (FARB) BAYER AG.
XX
PI Xiao Y;
XX
DR WPI; 2002-122283/16.
XX
PT Novel purified human eosinophil serine protease 1-like enzyme, useful for
identifying modulators of enzyme activity for treating Paget's disease,
osteoporosis, airway allergy, asthma.
XX
PS Disclosure; Fig 4; 131pp; English.
XX
CC The invention relates to a purified human eosinophil serine protease-1
CC (esp-1) like enzyme. Esp-1 like enzyme is useful in in-vitro or in-vivo
CC assays to identify test compounds with potential therapeutic or
CC diagnostic value. Esp-1-like enzyme modulator is useful for treating espi-
CC like enzyme dysfunction related diseases condition such as asthma, airway
CC allergy, chronic obstructive pulmonary disease (COPD) or osteoporosis.
CC Esp-1 like enzyme is also useful in diagnostic assays for detecting

CC diseases and abnormalities or susceptibility to diseases related to
 CC presence of mutations in the nucleic acid sequences which encode the
 CC enzyme. Pharmaceutical composition comprising esp-1 like enzyme is useful
 CC for treating dermatitis, Paget's disease, and preventing degradation of
 CC bone implants particularly dental implants. The present sequence is human
 CC esp-1 like enzyme
 XX
 XX Sequence 314 AA;

Query Match 96.4%; Score 1728; DB 5; Length 314;
 Best Local Similarity 100.0%; Pred. No. 5.8e-148;
 Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 14 MGARGALLALLARAGLRKPESQEAAPLSQPCRRVITSRVGGEDAEIGRWPMQGLR 73
 DB 1 MGARGALLALLARAGLRKPESQEAAPLSQPCRRVITSRVGGEDAEIGRWPMQGLR 60
 QY 74 LWDHVGVSVLSHRWALTAACPEYSDLSDPGMMVQFGLTSMPSFWSLQAYTRYF 133
 DB 61 LWDHVGVSVLSHRWALTAACPEYSDLSDPGMMVQFGLTSMPSFWSLQAYTRYF 120
 QY 134 VSNLYLSPRYLGNPSYDIALVKLSAPVYTKHQIPICLOASTFEFENRTDCWWTGNGYIK 193
 DB 121 VSNLYLSPRYLGNPSYDIALVKLSAPVYTKHQIPICLOASTFEFENRTDCWWTGNGYIK 180
 QY 194 EDEALPSPHTLQEQVVAIIINSMCNHLFLKYSFRKIDFGDMVCAGNAQGGKDACFGDSGG 253
 DB 181 EDEALPSPHTLQEQVVAIIINSMCNHLFLKYSFRKIDFGDMVCAGNAQGGKDACFGDSGG 240
 QY 254 PLACKNGLWYQIGVSVNGVCGCRPNRPVYTNISHFEWIKLMAQSGMSQDDPSWPLL 313
 DB 241 PLACKNGLWYQIGVSVNGVCGCRPNRPVYTNISHFEWIKLMAQSGMSQDDPSWPLL 300
 QY 314 FFPLLWALPLIGPV 327
 DB 301 FFPLLWALPLIGPV 314

RESULT 11

ABU71634
 ID ABU71634 standard; protein; 314 AA.

XX AC ABU71634;

XX DT 16-JUN-2003 (first entry)

XX DE Human PRO polypeptide #45.

XX Human; PRO; secreted polypeptide; transmembrane polypeptide;
 KW pathological disorder; cardiac insufficiency disorder; protein secretion;
 KW pancreas; diabetes; gastrointestinal mucosa; mucosal lesion; psoriasis;
 KW skin disease; keratinocyte differentiation; epithelial cancer; tumour;
 KW lung squamous cell carcinoma; epidermoid carcinoma; vulva; glioma;
 KW cytosstatic; cardiac; endocrine; antidiabetic; gastrointestinal;
 KW antiulcer; dermatological; vulnary.

XX OS Homo sapiens.

XX PN US2002146709-A1.

XX PD 10-OCT-2002.

XX PF 18-JUL-2001; 2001US-00909088.

XX PR 17-SEP-1997; 97US-0059113P.

XX PR 17-SEP-1997; 97US-0059115P.

XX PR 17-SEP-1997; 97US-0059117P.

XX PR 17-SEP-1997; 97US-0059119P.

XX PR 17-SEP-1997; 97US-0059121P.

XX PR 17-SEP-1997; 97US-0059122P.

XX PR 17-SEP-1997; 97US-0059184P.

XX PR 18-SEP-1997; 97US-0059263P.

XX PR 18-SEP-1997; 97US-0059266P.

PR 15-OCT-1997; 97US-0062125P.
 PR 17-OCT-1997; 97US-0062285P.
 PR 17-OCT-1997; 97US-0062287P.
 PR 21-OCT-1997; 97US-0063486P.
 PR 24-OCT-1997; 97US-0062814P.
 PR 24-OCT-1997; 97US-0062818P.
 PR 24-OCT-1997; 97US-0063045P.
 PR 24-OCT-1997; 97US-0063120P.
 PR 24-OCT-1997; 97US-0063121P.
 PR 24-OCT-1997; 97US-0063127P.
 PR 24-OCT-1997; 97US-0063128P.
 PR 27-OCT-1997; 97US-0063327P.
 PR 27-OCT-1997; 97US-0063329P.
 PR 28-OCT-1997; 97US-0063541P.
 PR 28-OCT-1997; 97US-0063542P.
 PR 28-OCT-1997; 97US-0063544P.
 PR 28-OCT-1997; 97US-0063549P.
 PR 28-OCT-1997; 97US-0063550P.
 PR 28-OCT-1997; 97US-0063564P.
 PR 29-OCT-1997; 97US-0063435P.
 PR 29-OCT-1997; 97US-0063704P.
 PR 29-OCT-1997; 97US-0063732P.
 PR 29-OCT-1997; 97US-0063734P.
 PR 29-OCT-1997; 97US-0063735P.
 PR 29-OCT-1997; 97US-0063738P.
 PR 31-OCT-1997; 97US-0064215P.
 PR 31-OCT-1997; 97US-0063870P.
 PR 31-OCT-1997; 97US-0064103P.
 PR 03-NOV-1997; 97US-0064248P.
 PR 07-NOV-1997; 97US-0064809P.
 PR 12-NOV-1997; 97US-0065186P.
 PR 17-NOV-1997; 97US-0065846P.
 PR 18-NOV-1997; 97US-0065693P.
 PR 21-NOV-1997; 97US-0066120P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 24-NOV-1997; 97US-0066453P.
 PR 24-NOV-1997; 97US-0066466P.
 PR 24-NOV-1997; 97US-0066511P.
 PR 24-NOV-1997; 97US-0066770P.
 PR 24-NOV-1997; 97US-0066772P.
 PR 10-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98WO-US019177.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98WO-US025108.
 PR 01-DEC-1998; 98WO-US025108.
 PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030895.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 2000WO-US000219.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00665550.
 PR XX
 PR XX
 PR XX

(GETH) GENENTECH INC.

PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Flvarcoff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin LJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX WPI; 2003-328338/31.
DR N-PSDB; ACA59107.
DR N-PSDB; ACA59107.
XX
XX Isolated nucleic acid useful for e.g., treating pathological disorders
PT encodes a secreted or transmembrane protein.
XX
XX Claim 12; Fig 92; 473pp; English.
XX
CC The invention relates to human PRO polypeptides (secreted or
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC PRO polypeptides and polynucleotides can be used in treating pathological
CC disorders and tumours, in therapeutic treatment of cardiac insufficiency
CC disorders and in therapeutic treatment of disorders involving protein
CC secretion by the pancreas, including diabetes. They can also be used in
CC treating disorders associated with the preservation and maintenance of
CC gastrointestinal mucosa and the repair of acute and chronic mucosal
CC lesions, and skin diseases associated with abnormal keratinocyte
CC differentiation (e.g., psoriasis, epithelial cancers such as lung
CC squamous cell carcinoma, epidermoid carcinoma of the vulva and gliomas).
CC The sequences can be used as molecular markers for protein
CC electrophoresis purposes and can be utilised in protein-protein binding
CC assays, biochemical screening assays, immunoassays and cell-based assays.
CC This sequence represents a human PRO polypeptide of the invention
XX
XX Sequence 314 AA;
SQ

Query Match 96.4%; Score 1728; DB 6; Length 314;
Best Local Similarity 100.0%; Pred. No. 5.8e-148;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 MGARGALLIALLARAGLRKPSQEAAPLSGCGRRVITSRIVGGEDAEIAGRPWQGSILR 73
Db 1 MGARGALLIALLARAGLRKPSQEAAPLSGCGRRVITSRIVGGEDAEIAGRPWQGSILR 60

QY 74 LMDSHVCGVLSLSHRWALTAACFCFETYSLDSPSGMWVQFGOLTSMPFWSLQAYTYRYF 133
Db 61 LMDSHVCGVLSLSHRWALTAACFCFETYSLDSPSGMWVQFGOLTSMPFWSLQAYTYRYF 120

QY 134 VSNIIYLSRYLGNPSYDIALVKLSAPVYTKHIQICLOASTFEFENRTDCWVTGWGIK 193
Db 121 VSNIIYLSRYLGNPSYDIALVKLSAPVYTKHIQICLOASTFEFENRTDCWVTGWGIK 180

QY 194 EDEALPSPTLQEVQVAIIINNSVCHLFLKYSFRKDIQDMVCAGNAQGGKDACFGDSGG 253
Db 181 EDEALPSPTLQEVQVAIIINNSVCHLFLKYSFRKDIQDMVCAGNAQGGKDACFGDSGG 240

QY 254 PLACNKNGLWYQIGVYVSWGVGGRPNRPGVYTNISHFEWIKLMAQSGMSQDPSPWPLL 313
Db 241 PLACNKNGLWYQIGVYVSWGVGGRPNRPGVYTNISHFEWIKLMAQSGMSQDPSPWPLL 300

QY 314 FPELLWALFLGVP 327
Db 301 FPELLWALFLGVP 314

RESULT 12
ABU71489
ID ABU71489 standard; protein; 314 AA.
AC
XX
XX ABU71489;
XX
XX
DT 10-JUN-2003 (first entry)
XX
XX Human PRO polypeptide #45.
DE
XX
XX Human; secreted and transmembrane protein; PRO polypeptide; cancer;
KW Alzheimer's disease; ischaemia; cytostatic; nootropic; vasotropic;
KW

KW neuroprotective.
XX
XX Homo sapiens.
XX
XX US2002192659-A1.
XX
XX 19-DEC-2002.
XX
XX 10-JUL-2001; 2001US-00902853.
XX
XX 17-SEP-1997; 97US-00591113P.
XX 17-SEP-1997; 97US-00591115P.
XX 17-SEP-1997; 97US-00591117P.
XX 17-SEP-1997; 97US-00591119P.
XX 17-SEP-1997; 97US-0059121P.
XX 17-SEP-1997; 97US-0059122P.
XX 17-SEP-1997; 97US-0059184P.
XX 18-SEP-1997; 97US-0059263P.
XX 18-SEP-1997; 97US-0059266P.
XX 15-OCT-1997; 97US-0062125P.
XX 17-OCT-1997; 97US-0062285P.
XX 17-OCT-1997; 97US-0062287P.
XX 21-OCT-1997; 97US-0063486P.
XX 24-OCT-1997; 97US-0062814P.
XX 24-OCT-1997; 97US-0062816P.
XX 24-OCT-1997; 97US-0063120P.
XX 24-OCT-1997; 97US-0063121P.
XX 24-OCT-1997; 97US-0063127P.
XX 24-OCT-1997; 97US-0063128P.
XX 27-OCT-1997; 97US-0063327P.
XX 27-OCT-1997; 97US-0063329P.
XX 28-OCT-1997; 97US-0063541P.
XX 28-OCT-1997; 97US-0063542P.
XX 28-OCT-1997; 97US-0063544P.
XX 28-OCT-1997; 97US-0063549P.
XX 28-OCT-1997; 97US-0063550P.
XX 28-OCT-1997; 97US-0063564P.
XX 29-OCT-1997; 97US-0063435P.
XX 29-OCT-1997; 97US-0063704P.
XX 29-OCT-1997; 97US-0063732P.
XX 29-OCT-1997; 97US-0063734P.
XX 29-OCT-1997; 97US-0063735P.
XX 29-OCT-1997; 97US-0063738P.
XX 29-OCT-1997; 97US-0064215P.
XX 31-OCT-1997; 97US-0063870P.
XX 31-OCT-1997; 97US-0064103P.
XX 03-NOV-1997; 97US-0064248P.
XX 07-NOV-1997; 97US-0064809P.
XX 12-NOV-1997; 97US-0065186P.
XX 17-NOV-1997; 97US-0065846P.
XX 18-NOV-1997; 97US-0065693P.
XX 21-NOV-1997; 97US-0066120P.
XX 21-NOV-1997; 97US-0066364P.
XX 24-NOV-1997; 97US-0066453P.
XX 24-NOV-1997; 97US-0066466P.
XX 24-NOV-1997; 97US-0066511P.
XX 24-NOV-1997; 97US-0066772P.
XX 24-NOV-1997; 97US-0066772P.
XX 10-SEP-1998; 98WO-US018824.
XX 14-SEP-1998; 98WO-US019177.
XX 16-SEP-1998; 98WO-US019330.
XX 17-SEP-1998; 98WO-US019437.
XX 01-DEC-1998; 98WO-US025108.
XX 08-SEP-1999; 99WO-US020594.
XX 13-SEP-1999; 99WO-US020944.
XX 15-SEP-1999; 99WO-US021090.
XX 15-SEP-1999; 99WO-US021547.
XX 05-OCT-1999; 99WO-US023089.
XX 29-NOV-1999; 99WO-US028214.
XX 30-NOV-1999; 99WO-US028313.
XX 01-DEC-1999; 99WO-US028301.
XX 02-DEC-1999; 99WO-US028564.

PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 30-MAR-2000; 2000WO-US007377.
 PR 20-MAR-2000; 2000WO-US008439.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 28-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00665350.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N,
 PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A,
 PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin LJ,
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D,
 PI Williams PM, Wood WI;
 XX WPI; 2003-361832/34.
 DR N-PSDB; ACAS8504.
 XX
 XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO245 or
 PT PRO1868, useful in molecular biology, chromosome and gene mapping, in
 PT generating antisense RNA and DNA, and in gene therapy.
 XX
 PS Claim 12; Fig 92; 474pp; English.
 XX
 CC The present invention relates to the isolation of novel human secreted
 CC and transmembrane proteins (PRO polypeptides), and the polynucleotide
 CC sequences encoding them. The polynucleotide sequences are useful in
 CC molecular biology, as hybridisation probes, in chromosome and gene
 CC mapping, in generating antisense RNA and DNA, and in gene therapy. The
 CC polynucleotide sequences may also be used in preparing PRO polypeptides
 CC by recombinant techniques, and in generating either transgenic animals or
 CC knock-out animals which, in turn, are useful in the development and
 CC screening of therapeutically useful reagents. The PRO polypeptides or
 CC their antibodies are useful in preparing a medicament for treating a
 CC condition responsive to the polypeptide or antibody, such as cancer,
 CC Alzheimer's disease or ischaemia, and in various diagnostic assays.
 CC ABU71445-ABU71505 represent human PRO polypeptides of the invention
 XX
 SQ Sequence 314 AA;
 Query Match 96.4%; Score 1728; DB 6; Length 314;
 Best Local Similarity 100.0%; Pred. No. 5.8e-148; Indels 0; Gaps 0;
 Matches 314; Conservative 0; Mismatches 0;
 QY 14 MGARGALLALLARAGLRKPESQEAAPLSGPGRRVITSRIVGGEDALGRWPGQSLR 73
 Db 1 MGARGALLALLARAGLRKPESQEAAPLSGPGRRVITSRIVGGEDALGRWPGQSLR 60
 QY 74 LWDSHVCGVSLSHRWALTAHCFETYSDLSDFSGWVWFQGLTSPSPFWSLQAYTRYF 133
 Db 61 LWDSHVCGVSLSHRWALTAHCFETYSDLSDFSGWVWFQGLTSPSPFWSLQAYTRYF 120
 QY 134 VSNILSPRYLGNSPYDIALVKLSAPVYTKHQICLOASTFEPENRTDCWVTGWGXYIK 193
 Db 121 VSNILSPRYLGNSPYDIALVKLSAPVYTKHQICLOASTFEPENRTDCWVTGWGXYIK 180
 QY 194 EDEALSPHTLOEQVAVINNSCNHLFLKYSFRKDI FGDWVCAGNAQGGKACFGDSGG 253
 Db 181 EDEALSPHTLOEQVAVINNSCNHLFLKYSFRKDI FGDWVCAGNAQGGKACFGDSGG 240
 QY 254 PLACNKNGLWYQLGVSWGVCGRPNRPGVYTNISHHFEWIKLMAQSGMSQDPDSWPLL 313
 Db 241 PLACNKNGLWYQLGVSWGVCGRPNRPGVYTNISHHFEWIKLMAQSGMSQDPDSWPLL 300

QY 314 FPPLWALPLIGPV 327
 Db 301 FPPLWALPLIGPV 314
 RESULT 13
 ABU71935
 ID ABU71935 standard; protein; 314 AA.
 XX
 AC ABU71935;
 XX
 DT 12-JUN-2003 (first entry)
 XX
 DE Human secreted/transmembrane protein PRO303.
 XX
 KW Human; secreted protein; transmembrane protein; PRO; gene therapy;
 KW chromosome identification; chromosome marker.
 XX
 OS Homo sapiens.
 PN US2003003530-A1.
 XX
 PD 02-JAN-2003.
 XX
 PF 11-JUL-2001; 2001US-00904011.
 XX
 PR 17-SEP-1997; 97US-0059113P.
 PR 17-SEP-1997; 97US-0059115P.
 PR 17-SEP-1997; 97US-0059117P.
 PR 17-SEP-1997; 97US-0059119P.
 PR 17-SEP-1997; 97US-0059121P.
 PR 17-SEP-1997; 97US-0059122P.
 PR 17-SEP-1997; 97US-0059184P.
 PR 18-SEP-1997; 97US-0059263P.
 PR 18-SEP-1997; 97US-0059286P.
 PR 15-OCT-1997; 97US-0062135P.
 PR 17-OCT-1997; 97US-0062285P.
 PR 17-OCT-1997; 97US-0062287P.
 PR 21-OCT-1997; 97US-0063486P.
 PR 24-OCT-1997; 97US-0062814P.
 PR 24-OCT-1997; 97US-0063045P.
 PR 24-OCT-1997; 97US-0063120P.
 PR 24-OCT-1997; 97US-0063121P.
 PR 24-OCT-1997; 97US-0063127P.
 PR 27-OCT-1997; 97US-0063327P.
 PR 27-OCT-1997; 97US-0063329P.
 PR 28-OCT-1997; 97US-0063541P.
 PR 28-OCT-1997; 97US-0063542P.
 PR 28-OCT-1997; 97US-0063544P.
 PR 28-OCT-1997; 97US-0063549P.
 PR 28-OCT-1997; 97US-0063550P.
 PR 28-OCT-1997; 97US-0063564P.
 PR 29-OCT-1997; 97US-0063435P.
 PR 29-OCT-1997; 97US-0063704P.
 PR 29-OCT-1997; 97US-0063732P.
 PR 29-OCT-1997; 97US-0063734P.
 PR 29-OCT-1997; 97US-0063735P.
 PR 29-OCT-1997; 97US-0063738P.
 PR 29-OCT-1997; 97US-0064215P.
 PR 31-OCT-1997; 97US-0064215P.
 PR 31-OCT-1997; 97US-0064248P.
 PR 03-NOV-1997; 97US-0064103P.
 PR 07-NOV-1997; 97US-0064809P.
 PR 12-NOV-1997; 97US-0065186P.
 PR 17-NOV-1997; 97US-0065846P.
 PR 18-NOV-1997; 97US-0065693P.
 PR 21-NOV-1997; 97US-0066120P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 24-NOV-1997; 97US-0066453P.
 PR 24-NOV-1997; 97US-0066646P.


```
PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
PR 21-OCT-1997; 97US-0062287P.
PR 24-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 01-DEC-1998; 98WO-US025108.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX PA
(GETH ) GENENTECH INC.
```

```
XX Ashkenazi A, Botstein D, Desnovers L, Eaton DL, Ferrara N,
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A,
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ,
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D,
XX Williams PM, Wood WI,
DR WPI; 2003-370793/35.
XX N-PSDB; ACD07611.
```

New Genes and secreted and transmembrane polypeptides (e.g. PRO245 or PRO335), useful for treating or diagnosing e.g. Alzheimer's disease, cancers, hemorrhage, rheumatoid arthritis, diabetes, cirrhosis, ischemia or strokes.

Claim 12; Fig 92; 482pp; English.

The invention describes a new isolated nucleic acid molecule comprising the full length coding sequence of the DNA deposited with the American Type Culture Collection (e.g. ATCC Deposit No. 209258), or a sequence with at least 80% identity to a DNA encoding a PRO polypeptide comprising any of 61 sequences having 184-119 amino acids fully defined in the specification. The PRO polypeptides or polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These are particularly useful for detecting or treating e.g. Parkinson's disease, Alzheimer's disease, inflammations, nephritis, wound healing, nerve repair, collateral blood vessel formation, cancers (e.g. colorectal cancer), haemorrhage (or reduce risk for haemorrhage), rheumatoid arthritis, diabetes, cirrhosis of the liver, fibrosis of the lungs, restenosis, dermal fibrotic conditions (e.g. keloids or scarring), ischaemia, strokes, hypertension, heart attacks, atherosclerosis, or infertility in mammals (e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats, or rabbits). The PRO polypeptides are useful as targets for therapeutic intervention in these diseases, and diagnostic determination of the presence of these diseases. The PRO polypeptides are also useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. This is the amino acid sequence of a novel human secreted and transmembrane PRO polypeptide

Sequence 314 AA;

Query Match 96.4%; Score 1728; DB 6; Length 314;
Best Local Similarity 100.0%; Pred. No. 5.8e-148;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 MGARGALLALLARAGLRKPESEAPLSGPCGRVITSRVGGEDALGRWPQGSRLR 73

Db 1 MGARGALLALLARAGLRKPESEAPLSGPCGRVITSRVGGEDALGRWPQGSRLR 60

QY 74 LWDSHVCGVSLLSHRWALTAHCFETYSDLSDPSGMWVFGQLTSMPSFWSLQAYTRYF 133

Db 61 LWDSHVCGVSLLSHRWALTAHCFETYSDLSDPSGMWVFGQLTSMPSFWSLQAYTRYF 120

QY 134 VSNIIYSPRYLGNSPYDIALVKLSAPVYTKHIQICLOASTFEPENRDCWVTGWGYIK 193

Db 121 VSNIIYSPRYLGNSPYDIALVKLSAPVYTKHIQICLOASTFEPENRDCWVTGWGYIK 180

QY 194 EDEALPSPHTLQEVQVAIINNMCNHLFLKYSPRKDFGDMVCAGNAQGGKACFGDSGG 253

Db 181 EDEALPSPHTLQEVQVAIINNMCNHLFLKYSPRKDFGDMVCAGNAQGGKACFGDSGG 240

QY 254 PLACNKNGLWYQIGVSVGWGCGRPNRPGVYTNISHHFEWIKMLAQSGMSQDPDPWPLL 313

Db 241 PLACNKNGLWYQIGVSVGWGCGRPNRPGVYTNISHHFEWIKMLAQSGMSQDPDPWPLL 300

QY 314 FFPLLWALPLLGPV 327

Db 301 FFPLLWALPLLGPV 314

RESULT 15

ABU54391
ID ABU54391 standard; protein; 314 AA.
XX AC ABU54391;
XX DT 10-MAR-2003 (first entry)
XX DE Human secreted/transmembrane protein PRO303.
XX KW Human; PRO; secreted protein; transmembrane protein; enterocolitis;
KW Gastrointestinal ulceration; skin disease;
KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
KW squamous cell carcinoma; Alzheimer's disease; Parkinson's disease;
KW amyotrophic lateral sclerosis; inflammatory disease;
KW rheumatoid arthritis; asthma; multiple sclerosis;
KW atherosclerosis; cardiac injury; infertility; organ failure;
KW premature aging; AIDS; acquired immunodeficiency syndrome; cancer;
KW diabetic complication; wound repair.
XX OS Homo sapiens.
XX PN US2002132240-A1.
XX PD 19-SEP-2002.
XX PF 18-JUL-2001; 2001US-00909320.
XX 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 18-SEP-1997; 97US-0062125P.
PR 18-SEP-1997; 97US-0062285P.
PR 18-SEP-1997; 97US-0062287P.
PR 18-SEP-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063341P.
PR 28-OCT-1997; 97US-0063342P.
PR 28-OCT-1997; 97US-0063344P.
PR 28-OCT-1997; 97US-0063349P.
PR 28-OCT-1997; 97US-0063350P.
PR 28-OCT-1997; 97US-0063356P.
PR 28-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0065120P.
PR 21-NOV-1997; 97US-0065364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.

PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 01-DEC-1998; 98WO-US025108.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 06-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX (GETH) GENENTECH INC.
XX PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ,
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
XX Williams PM, Wood WI;
DR WPI; 2003-147434/14.
DR N-PSDB; ABX71659.
XX New PRO polypeptides and nucleic acid molecules, useful in diagnosing or
PT treating inflammatory diseases, organ failure, atherosclerosis, cardiac
PT injury, infertility, cancer, AIDS, Alzheimer's disease or Parkinson's
XX disease.
PS Claim 12; Fig 92; 473pp; English.
XX The invention relates to an isolated PRO polypeptide having at least 80%
CC amino acid sequence identity to: (a) any one of 61 fully defined amino
CC acid sequences given in the specification (appearing as ABU54347-
CC ABU54407); (b) an amino acid sequence encoded by the nucleotide sequence
CC deposited under American Type Culture Collection (accession numbers
CC listed in the specification); (c) any one of the PRO sequences which
CC lacks its associated signal peptide; (d) an extracellular domain of the
CC PRO polypeptide with its associated signal peptide; or (e) an
CC extracellular domain of the PRO polypeptide which lacks its associated
CC signal peptide. Also include are the nucleic acids encoding the PRO
CC polypeptides, vectors, host cells and anti-PRO antibodies. The PRO
CC polypeptides and nucleic acids are useful in diagnosing or treating
CC enterocolitis, gastrointestinal ulceration, skin diseases associated with
CC abnormal keratinocyte differentiation, e.g. psoriasis or epithelial
CC cancers such as squamous cell carcinoma, Alzheimer's disease, Parkinson's
CC disease, amyotrophic lateral sclerosis, inflammatory diseases, e.g.
CC rheumatoid arthritis, asthma or multiple sclerosis, organ failure,
CC atherosclerosis, cardiac injury, infertility, birth defects, premature
CC aging, AIDS, cancer, diabetic complications, or mutations in general. The
CC polypeptides are also useful for wound repair and associated therapies
CC concerned with re-growth of tissue. The nucleotide sequences may be used

CC as hybridisation probes in chromosome and gene mapping, or in generating
CC antisense RNA and DNA. PRO nucleic acids are also useful in preparing PRO
CC polypeptides, in assays to identify other proteins or molecules involved
CC in binding reaction, to generate transgenic animals or knockout animals,
CC which in turn are useful in the development and screening of
CC therapeutically useful reagents, for chromosome identification, and
CC tissue typing. The PRO polypeptides and nucleic acid molecules are also
CC useful in gene therapy, and as molecular weight markers for protein
CC electrophoresis purposes. The anti-PRO antibodies may be used in
CC diagnostic assays for PRO, or for the affinity purification of PRO from
CC recombinant cell culture or natural sources. The present sequence
CC represents a PRO polypeptide
XX
SQ Sequence 314 AA;

Query Match 96.4%; Score 1728; DB 6; Length 314;
Best Local Similarity 100.0%; Pred. No. 5.8e-148;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 MCARGALLALLARAGLRKPESQEAAPLSGCGRRVITSRIVGGEDELGRWPQGSRLR 73
DB 1 MCARGALLALLARAGLRKPESQEAAPLSGCGRRVITSRIVGGEDELGRWPQGSRLR 60
QY 74 LWDHVGCVSLLSHRWALTAHCFETYSDLSDPGVMVQFQOLTSMPFSWLSQAYTRYF 133
DB 61 LWDHVGCVSLLSHRWALTAHCFETYSDLSDPGVMVQFQOLTSMPFSWLSQAYTRYF 120
QY 134 VSNIVLSPRYLGNSPYDIALVKLSAPVYTYKHQIPICIQASTFEFENRTDCWVTGMYIK 193
DB 121 VSNIVLSPRYLGNSPYDIALVKLSAPVYTYKHQIPICIQASTFEFENRTDCWVTGMYIK 180
QY 194 EDEALPSPHTLQEVQVAIINNMCNHLFLKYSFRKIDFGDMVCAGNAQGGKDACFGDSGG 253
DB 181 EDEALPSPHTLQEVQVAIINNMCNHLFLKYSFRKIDFGDMVCAGNAQGGKDACFGDSGG 240
QY 254 PLACNKGWLWYQIGVSVGCGRENRPQVYTNISHHFEWIKLMAQSGMSQDPDPSPWPLL 313
DB 241 PLACNKGWLWYQIGVSVGCGRENRPQVYTNISHHFEWIKLMAQSGMSQDPDPSPWPLL 300
QY 314 PFPLLWALPLGPV 327
DB 301 PFPLLWALPLGPV 314

Search completed: April 6, 2004, 14:11:37
Job time : 61 secs

GenCore version S.i.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2004, 14:09:59 ; Search time 20 Seconds
(without alignments)
1572.731 Million cell updates/sec

Title: US-09-787-844-2
Perfect score: 1792
Sequence: 1 RRQRGRQAGEEAMGARGAL.....PSWPLLPFLMLWLPILGPV 327

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:
1: p1r1:
2: p1r2:
3: p1r3:
4: p1r4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	580	32.4	343	1 A57014	proctasin (EC 3.4.21.1) precursor - human
2	528.5	29.5	270	2 S56160	mast cell tryptase
3	518	28.9	275	2 C35863	tryptase (EC 3.4.21.1)
4	515	28.7	275	2 A35863	tryptase (EC 3.4.21.1)
5	514.5	28.7	638	1 KQMSPL	plasma kallikrein
6	514	28.7	275	2 B35863	tryptase (EC 3.4.21.1)
7	513	28.6	638	1 KQHUP	plasma kallikrein
8	512	28.6	276	2 A36554	mast cell protease
9	511	28.5	275	2 A32410	tryptase (EC 3.4.21.1)
10	511	28.5	638	1 KQRTPL	plasma kallikrein
11	507	28.3	273	2 A47246	tryptase (EC 3.4.21.1)
12	503.5	28.1	274	2 A45754	tryptase (EC 3.4.21.1)
13	500	27.3	274	2 JCA171	tryptase (EC 3.4.21.1)
14	483.5	27.0	625	1 KFHU1	coagulation factor
15	477.5	26.6	417	1 S08845	hepsin (EC 3.4.21.1)
16	475.5	26.5	366	2 JE0105	testicular serine
17	456.5	25.5	237	2 S68702	tryptase (EC 3.4.21.1)
18	455.5	25.4	415	1 A34170	tryptase (EC 3.4.21.1)
19	455.5	25.4	810	1 PLHU	acrosin (EC 3.4.21.1)
20	454	25.3	455	2 A61545	plasmin (EC 3.4.21.1)
21	452.5	25.3	436	2 JX0172	acrosin (EC 3.4.21.1)
22	449	25.1	955	2 JC7731	membrane-bound arg
23	448.5	25.0	367	2 JE0104	testicular serine
24	447	24.9	416	1 S33777	hepsin (EC 3.4.21.1)
25	446.5	24.9	421	2 S29599	acrosin (EC 3.4.21.1)
26	446	24.9	1035	1 A40390	enteropeptidase (E
27	444.5	24.8	4548	1 S0657	apoptein(a)
28	444	24.8	1113	2 JE0315	low-density lipopr
29	443	24.7	1019	1 A56318	enteropeptidase (E

30	439.5	24.5	418	2 A37344	acrosin (EC 3.4.21.1)
31	437.5	24.4	460	2 B61545	plasmin (EC 3.4.21.1)
32	436	24.3	810	2 B30848	plasmin (EC 3.4.21.1)
33	435.5	24.3	431	2 S47538	acrosin (EC 3.4.21.1)
34	435.5	24.3	790	1 PLPG	plasmin (EC 3.4.21.1)
35	435.5	24.3	812	1 PLMS	plasmin (EC 3.4.21.1)
36	433	24.2	812	1 PLBO	plasmin (EC 3.4.21.1)
37	430.5	24.0	437	2 S18407	acrosin (EC 3.4.21.1)
38	430	24.0	421	1 S11674	acrosin (EC 3.4.21.1)
39	430	24.0	786	1 A47547	acrosin (EC 3.4.21.1)
40	428.5	23.9	265	2 S54146	serine proteinase
41	428	23.9	810	2 I46260	trypsin (EC 3.4.21.1)
42	427	23.8	1420	2 A32859	plasmin (EC 3.4.21.1)
43	422	23.5	1524	2 T30337	apolipoprotein(a)
44	417	23.3	1034	1 A53663	polyprotein - Afri
45	414	23.1	269	2 B32410	enteropeptidase (E
					mastocytoma protei

ALIGNMENTS

RESULT 1

A57014
proctasin (EC 3.4.21.1) precursor - human
C:Species: Homo sapiens (man)
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 21-Apr-2003
C:Accession: A57014; A54866
R:Yu, J.X.; Chao, L.; Chao, J.
J. Biol. Chem. 270, 13483-13489, 1995
A:Title: Molecular cloning, tissue-specific expression, and cellular localization of hu
A:Reference number: A57014; MUID:95286644; PMID:7768952
A:Accession: A57014
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-343 <RES>
A:Cross-references: GB:L41351; NID:G862304; PIDN:AAC41759.1; PID:G862305
A:Experimental source: prostate
A:Note: parts of this sequence were determined by protein sequencing
R:Yu, J.X.; Chao, L.; Chao, J.
J. Biol. Chem. 269, 18843-18848, 1994
A:Title: Proctasin is a novel human serine proteinase from seminal fluid. Purification,
A:Reference number: A54866; MUID:94308140; PMID:8034638
A:Accession: A54866
A:Molecule type: protein
A:Residues: 45-64 <YUA>
C:Genetics:
C:Gene: GDB:PRSS8
A:Cross-references: GDB:676446; OMIM:600823
A:Map position: 16p11.2-16p11.2
C:Superfamily: trypsin; trypsin homology
C:Keywords: glycoprotein; hydrolase; serine proteinase; transmembrane protein
F:33-44 45-343/Product: proctasin #status predicted <MAT>
F:33-44/Domain: signal sequence #status predicted <CHL>
F:45-343/Domain: proctasin light chain #status predicted <CHL>
F:45-281/Domain: trypsin heavy chain #status predicted <CHH>
F:323-341/Domain: trypsin homology #TRY>
F:323-341/Domain: transmembrane #status predicted <TM1>
F:37-154,70-86,168-244,201-223,234-262/Disulfide bonds: #status predicted
F:85,134,238/Active site: His, Asp, Ser #status predicted
F:159/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 32.4%; Score 580; DB 1; Length 343;
Best Local Similarity 40.6%; Pred. No. 3.7e-44;
Matches 146; Conservative 47; Mismatches 107; Indels 60; Gaps 14;

Qy	3	ORGRQAAGEAMGARGALLALLARAGLRKPSQEAAPLSGPCGRRVITSRVGGEDAE 62
Db	3	QKGVLPFGQ--LGA-VALLYLGLLRSG-TGAEGAA-----PCG-VAQARTTGSSAV 52
Qy	63	LGRWPWGSLRLWDSHVGCVSLSHRWALTAHCFETYSDLSDPS-----GMWVQFG--Q 115
Db	53	AGQWPQWQSVITBEGHVGCGSLVSEQWLSAAHCF-----PSEHKEAYEVKLGAHQ 104

J. Biol. Chem. 262, 1363-1373, 1987
A;Title: Human pituitary trypsin: molecular forms, NH-2-terminal sequence, immunocytochemistry
A;Reference number: A39326; MUID:87109258; PMID:3543004
A;Accession: A39326
A;Molecule type: protein
A;Residues: 31-38 <CRO>
A;Experimental source: pituitary
C;Genetics:
A;Intons: 21/1; 78/2; 177/1; 221/3
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase; zymogen
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-30/Domain: activation peptide #status predicted <ACT>
F;31-275/Product: trypsin I #status experimental <MAY>
F;31-267/Domain: trypsin homology <TRY>
F;74,121,224/Active site: His, Asp, Ser #status predicted

Query Match 28.7%; Score 515; DB 2; Length 275;
Best Local Similarity 40.3%; Pred. No. 1.9e-38;
Matches 116; Conservative 42; Mismatches 92; Indels 38; Gaps 11;
QY 20 LLLAL--LLARAGLRKPSQEAAPISGCGRRVITSIRVIGGEDAELGRWPQGSURL--- 74
DB 5 LLLALPVLASRA-----YAAPAGQALQV---GIVGQEAAPRSKWPQVSLRVHGP 53
QY 75 -KDSHVCVSLSHRWALTAACHCFETYSDLSPPSCMWVQFGLTSMPSFWSLQAYTRYF 133
DB 54 YR-MHFCGSLHPQVLTAAHC--VGPDVKDLAALRVQLRE-----CHLYYQDL 101
QY 134 --VSNIIYSPR-YLGNSPYDIALVKSAPVTVTKHIQICLQASTFEFENRTDCWVTGWG 190
DB 102 LPVSRIIVHPQYTAQIGADIALLEBPVNVSSHVHTVTPPASETTPPGMPCWVTGWG 161
QY 191 YKEDALPSPHTLQEVQVAIINNSMCHLFLKYSFRD----IFGDMVCAGNAGQGGDA 246
DB 162 DVDNDRUPPPPLKQVQKVPINENICDAKHLGALGDDVRIVRDDMLCAGNTR--RDS 219
QY 247 CFGDSGGPLACNKGILWQIGVSVGCGRRNRGVTNISHPEWI 294
DB 220 CQDGGGFLVCKVNTWLAGVSVGEGCAQPNRGITRYTYILDWI 267

RESULT 5
KQMSPL
A;Title: Mouse plasma kallikrein (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 18-Jun-1999
C;Accession: A36557
R;Seidah, N.G.; Sawyer, N.; Hamelin, J.; Mion, P.; Beaubien, G.; Brachpapa, L.; Rochemont
DNA Cell Biol. 9, 737-748, 1990
A;Title: Mouse plasma kallikrein: cDNA structure, enzyme characterization, and comparison
A;Reference number: A36557; MUID:91090844; PMID:2264928
A;Molecule type: mRNA
A;Accession: A36557
A;Residues: 1-638 <SEI>
A;Cross-references: GB:M59586; NID:g200358; PIDN:AAA63393.1; PID:g200359
A;Note: part of this sequence, including the amino ends of both the heavy and light chain
C;Comment: This protein, synthesized in the liver, circulates as a noncovalent complex with
are linked by one or more disulfide bonds.
C;Superfamily: coagulation factor XI; trypsin homology
C;Keywords: blood coagulation; duplication; fibrinolysis; glycoprotein; hydrolase; infla
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-390/Product: plasma kallikrein heavy chain #status experimental <HCH>
F;20-109/Domain: apple repeat <AP1>
F;110-199/Domain: apple repeat <AP2>
F;200-289/Domain: apple repeat <AP3>
F;291-380/Domain: apple repeat <AP4>
F;391-638/Product: plasma kallikrein light chain #status experimental <LCH>
F;391-621/Domain: trypsin homology <TRY>
F;21-104;47-77;51-57;111-194;137-166;141-147;201-284;227-256;231-237;292-375;318-347;322
F;127,215,308,396,494/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;434,483,578/Active site: His, Asp, Ser #status predicted

Query Match 28.7%; Score 514.5; DB 1; Length 638;
Best Local Similarity 40.2%; Pred. No. 5.8e-38;
Matches 101; Conservative 43; Mismatches 84; Indels 23; Gaps 8;
QY 51 ITSRIVGEDAEELGRWPQGSRL---LWDSHVCVSLSHRWALTAACHCFE--TYSDLS 105
DB 387 INARIIVGGTNASLGEPWQVSLQVLSQTHLCGSGIQRQWYLTAAHCFDGIPIPDVVR 446
QY 106 PSGMWVQFGOLT-SMPSFWSLQAYTRYFVSNIIYLSPRY-LGNSPYDIALVKSAPVTVT 163
DB 447 IYGGILLSLSITKETS-----SR--IKELIIHQEYKVSSEGYDIALIKLQTLNYT 496
QY 164 KHQPCICLQASTFEFENRTDCWVTGNGYIKEDALPSPHTLQEVQVAIINNSMCHLFLK 223
DB 497 EFQKPICLPSKADTNTIYNCWVTGNGYTKEQG--ETQNILOKATPLFVNESECQKYRD 554
QY 224 YSPRKDIFGDMVCAGNAGGKDACFGDSGGPLVCKHGRVQLVGIISWEGCGRKQDPGV 293
DB 555 YVINK-----QMICAGYKEGGTDACKSDSGGFLVCKHGRVQLVGIISWEGCGRKQDPGV 610
QY 284 YTNISHFEWI 294
DB 611 YTKVSEYMDWI 621

RESULT 6
B35863
A;Title: II precursor - human
N;Alternate names: trypsinase beta
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C;Accession: B35863; A37193; I59473
R;Vandarslice, P.; Ballinger, S.M.; Tam, E.K.; Goldstein, S.M.; Craik, C.S.; Caughey, G
Proc. Natl. Acad. Sci. U.S.A. 87, 3811-3815, 1990
A;Title: Human mast cell trypsinase: multiple cDNAs and genes reveal a multigene serine p
A;Reference number: A35863; MUID:90251647; PMID:2187193
A;Accession: B35863
A;Molecule type: mRNA; DNA
A;Residues: 1-275 <VAN>
A;Cross-references: GB:M33492; NID:g339982; PIDN:AAA36779.1; PID:g339983
A;Note: residues 2-275 are derived from mRNA; residue one was inferred from the genomic
R;Miller, J.S.; Moxley, G.; Schwartz, L.B.
J. Clin. Invest. 86, 864-870, 1990
A;Title: Cloning and characterization of a second complementary DNA for human trypsinase.
A;Reference number: A37193; MUID:90369005; PMID:2203827
A;Accession: A37193
A;Molecule type: mRNA
A;Residues: 1-275 <MIL>
A;Cross-references: GB:M37488; NID:g179583; PIDN:AAA51843.1; PID:g179584
R;Blom, T.; Hellman, L.
Scand. J. Immunol. 37, 203-208, 1993
A;Title: Characterization of a trypsinase mRNA expressed in the human basophil cell line
A;Reference number: I59473; MUID:93166209; PMID:8434231
A;Accession: I59473
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-275 <RES>
A;Cross-references: GB:S5551; NID:g265666; PIDN:AAD13876.1; PID:g4261576
A;Experimental source: basophil cell line KU812
C;Genetics:
A;Gene: GDB:TPS1
A;Cross-references: GDB:125890; OMIM:191080
A;Map position: 16pter-16qter
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase; zymogen
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-30/Domain: activation peptide #status predicted <ACT>
F;31-267/Domain: trypsin I #status predicted <MAY>
F;74,121,224/Active site: His, Asp, Ser #status predicted

Query Match 28.7%; Score 514; DB 2; Length 275;

Best Local Similarity 40.3%; Pred. No. 2.3e-38;
Matches 116; Conservative 42; Mismatches 92; Indels 38; Gaps 11;
QY 20 LLAL--LLARAGLRKPESQEAAPLSGCGRRVITTSIVGGEDAEGLRNPWQGSRL-- 74
DB 5 LLLALPVLASRA-----YAPAPQALQRV---GIVGQAPSKPFWQVSLVHVP 53
QY 75 -WDSHVCVSLLSHRWALTAACHPETYSDLSDPSGMMVQFGQJLTSMPFSLQAYTRYF 133
DB 54 YW-MHFCGSLIHPQWLTAAHC--VGPDKDLAALRVQLRE-----QHLYYQDQL 101
QY 134 --VSNIVLSR- YLGNSPYDIALVKLSAPVYTKHQIPICLOASTFEFENRTDCWTG 190
DB 102 LPVSRIVHQFYTAQIGALIALEELPVPVSHVHTVLPFASFTPPGMPFCWTG 161
QY 191 YIKDEALPSPHTLQEVQVAIINNSMCNHLFLKYSFRK----IFGDMVCAGNAQGD 246
DB 162 DVDNDELRPLFPKQVKVPMENHICDAKYHLGAYTGDDVRIVRDMLCAGNTR--RDS 219
QY 247 CFCGSGGLACNKNGLWYQIGVSWGVCGRPNRPVYTNISHHFEWI 294
DB 220 CQGSGLPVCVNGTGLQAGVSWGEGCAQPNRPGIYTRYVYLDWI 267

RESULT 7
KOHUP
Plasma kallikrein (EC 3.4.21.34) precursor - human
N/A
C/Species: Homo sapiens (man)
C/Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 18-Jun-1999
C/Accession: A00921; A37939
R/Chung, D.W.; Fujikawa, K.; McMullen, B.A.; Davie, E.W.
Biochemistry 25, 2410-2417, 1986
A/Title: Human plasma prekallikrein, a zymogen to a serine protease that contains four
A/Reference number: A00921; MUID:86243359; PMID:3521732
A/Accession: A00921
A/Molecule type: mRNA
A/Residues: 1-638 <CHU>
A/Cross-references: GB:ML1343; NID:G190262; PIDN:AAA60153.1; PID:G190263
R/McMullen, B.A.; Fujikawa, K.; Davie, E.W.
Biochemistry 30, 2050-2056, 1991
A/Title: Location of the disulfide bonds in human plasma prekallikrein: the presence of
A/Reference number: A37939; MUID:91152016; PMID:1998666
A/Accession: A37939
A/Molecule type: protein
A/Residues: 20-27;40-46,'X',48,'H',50,'X',52-70,'H',75-76,'X',78-80;103-113;131-140;141-
260;283,'X',285-287;291,'X',293-295;314-317,'X',319-320;321-324,'X',329-333;334-339,'X',
525;538-551;562,'X',564-567;573,'X',575-576;578-583,'X',585;592-604 <MCM>
C/Comment: This protein, synthesized in the liver, circulates as a noncovalent complex
are linked by one or more disulfide bonds.
C/Comment: The enzyme cleaves Lys-Arg and Arg-Ser bonds. It activates, in a reciprocal
inogen and may also play a role in the renin-angiotensin system by converting prorenin
C/Genetics:
A/Gene: GDB:KLK3
A/Cross-references: GDB:127575; OMIM:229000
A/Map position: 4q35-4q35
C/Superfamily: coagulation factor XI; trypsin homology
C/Keywords: blood coagulation; duplication; fibrinolysis; glycoprotein; hydrolase; infla
F/1-19/Domain: signal sequence #status predicted <SIG>
F/20-638/Product: plasma kallikrein #status predicted <MAT>
F/20-390/Domain: plasma kallikrein heavy chain #status predicted <HCH>
F/20-109/Domain: apple repeat <AP1>
F/20-199/Domain: apple repeat <AP2>
F/200-289/Domain: apple repeat <AP3>
F/291-380/Domain: apple repeat <AP4>
F/391-638/Domain: plasma kallikrein light chain #status predicted <LCH>
F/391-621/Domain: trypsin homology <TRY>
F/21-104;47-77,51-57,111-194,137-166;141-147,201-284,227-256,231-237,292-375,322-328,383
F/127,308,396,453;494/Banding site: carbohydrate (Asn) [covalent] #status experimental
F/148-347;340-345/Disulfide bonds: #status predicted
F/390-391/Cleavage site: Arg-Ile [coagulation factor XIa] #status predicted
F/434,483,578/Active site: His, Asp, Ser #status predicted

Query Match 28.6%; Score 513; DB 1; Length 638;
Best Local Similarity 37.5%; Pred. No. 7.8e-38;
Matches 114; Conservative 45; Mismatches 103; Indels 42; Gaps 11;
QY 13 AMGARGALLALLARAGLRKPESQEAAPLSGCGRRVITTSIVGGEDAEGLRNPWQGS 72
DB 361 AYTQSGSGYSLRLCNTG-----DNSVCTTKTST-RIVGGTNSGEMWQVSL 408
QY 73 RL--WDSHVCVSLLSHRWALTAACHPETYSDLSDPSGMMVQFG-----OLTSMP 124
DB 409 QVKLTAQRHLCCGSLIGHQWLTAAHCFD---GLPLQDVWRIYSGILNLSITKDT 465
QY 135 IQ--AYTRYFVSNILSPRYLGNSPYDIALVKLSAPVYTKHQIPICLOASTFEFEN 182
DB 466 IKETIIHONYKSE-----GN--HDIALIKLQAPLNYTEFOKPICLPSKGTSTIYT 515
QY 183 DOWTGWYIKEDALPSPHTLQEVQVAIINNSMCNHLFLKYSFRKDFGDMVCAGNAQ 242
DB 516 NCWTGNGFSKEKEI--QNILQKNIPLVNTECQKRYQDYK----ITQRMVCA 569
QY 243 GKDACFGDSGGPLACNKNGLWYQIGVSWGVCGRPNRPVYTNISHHFEWI-QKLMA 301
DB 570 GKDACGDSGGPLVCXKNGMWRLVGITSWGEGCARREQPGVYTKVAEYMDWILEK 629
QY 302 GMSQ 305
DB 630 GRAQ 633

RESULT 8
A38654
mast cell proteinase 6 (EC 3.4.21.-) precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 21-Feb-1992 #sequence_revision 17-Feb-1994 #text_change 22-Jun-1999
C/Accession: A38654; B38654; D35646; I59478
R/Reynolds, D.S.; Gurley, D.S.; Austen, K.F.; Serafin, W.E.
J. Biol. Chem. 266, 3847-3853, 1991
A/Title: Cloning of the cDNA and gene of mouse mast cell protease-6. Transcription by
A/Reference number: A38654; MUID:91139682; PMID:1995638
A/Accession: A38654
A/Molecule type: DNA
A/Residues: 1-276 <REY>
A/Cross-references: GB:M57625; NID:G200506; PIDN:AAA39987.1; PID:G200507
s Gly. GAG for residue 148 as Gly, GAG for residue 168 as Gly, and GAA for 185 as Gly
A/Accession: B38654
A/Molecule type: mRNA
A/Residues: 1-276 <RE2>
A/Cross-references: GB:M57626; NID:G200508; PIDN:AAA39988.1; PID:G200509
R/Reynolds, D.S.; Stevens, R.L.; Lane, W.S.; Carr, M.H.; Austen, K.F.; Serafin, W.E.
Proc. Natl. Acad. Sci. U.S.A. 87, 3230-3234, 1990
A/Title: Different mouse mast cell populations express various combinations of at least
A/Reference number: A35646; MUID:90222202; PMID:2326280
A/Accession: D35646
A/Molecule type: protein
A/Residues: 32-54 <RE3>
R/Huang, R.; Abrink, M.; Gobl, A.E.; Nilsson, G.; Aveskog, M.; Larsson, L.G.; Nilsson,
Scand. J. Immunol. 38, 359-367, 1993
A/Title: Expression of a mast cell tryptase in the human monocytic cell lines U-937 and
A/Reference number: I59478; MUID:94023807; PMID:8210998
A/Accession: I59478
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-276 <RES>
A/Cross-references: GB:L31853; NID:G473480; PIDN:AAA39725.1; PID:G473481
C/Genetics:
A/Gene: MIM:6
A/Introns: 24/1, 79/2, 168/1, 222/3
C/Superfamily: trypsin; trypsin homology
C/Keywords: hydrolase; serine proteinase; zymogen
F/1-21/Domain: signal sequence #status predicted <SIG>
F/22-31/Domain: activation peptide #status predicted <ACT>

F;32-276/Product: mast cell proteinase 6 #status experimental <MAT>
F;32-268/Domain: trypsin homology <TRY>
F;75,122,225/Active site: His, Asp, Ser #status predicted

Query Match 28.6%; Score 512; DB 2; Length 276;
Best Local Similarity 39.3%; Pred. No. 3.5e-38;
Matches 106; Conservative 42; Mismatches 88; Indels 34; Gaps 9;
QY 45 PCGRVITSRIVGDEALGRWPQGSRLRL----WDSHVGCVSLSHRWALTAACFETY 100
DB 25 PANQRV---GIVGGEASESKWQVSLRFLKNY--IHFCCGSLIHPQWVLTAAFCVGP 80
QY 101 SLDSPSGMVQFQGLTSMPSFWSLQAYTRY-----FVSNIVLSR-PLGNSPYIALV 154
DB 81 --IKSPQLFRVQ-----LRQYLYVQDLSLNRVIVHPPHYTAEGGADVALL 126
QY 155 KLSAPVYTKHIQICLOASTFEFENRTDCWVTGWYKEDALPSPHTIQEYQVAINN 214
DB 127 ELEVPNVVSTHIHPISLPASSETFPCTSCWVTGWDINDDEPLPPYPLKQVKVIVEN 186
QY 215 SMCNHFLKYSFRKDIK----GDMVCAGNAGCGKACGDSGGPLACNKNGLWYQIGVVS 270
DB 187 SLCDRKHTGLTYGDDPFIVHDGMLCAGNTR--RDSQGSQSGGLVCKVKGTLQAGVVS 244
QY 271 WVGCGGRPNRPGVYTNLSHHFEWIKLMAQ 300
DB 245 WGECAQPNREGIYTRYIYLDIHRVPE 274

RESULT 9
A32410
C;Title: trypsin (EC 3.4.21.59) precursor - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 22-Jun-1999
C;Accession: A32410
R;Vanderslice, P.; Craik, C.S.; Nadel, J.A.; Caughey, G.H.
Biochemistry 28, 4148-4155, 1989
A;Title: Molecular cloning of dog mast cell tryptase and a related protease: structural
A;Reference number: A32410; MUID: 99352460; PMID: 2504277
A;Accession: A32410
A;Molecule type: mRNA
A;Residues: 1-275 <GAN>
A;Cross-references: GB:M24664; NID:G163982; PIDN:AAA30854.1; PID:G163983; GB:J02862
C;Superfamily: trypsin, trypsin homology
C;Keywords: hydrolase; serine proteinase; zymogen
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-30/Domain: activation peptide #status predicted <ACT>
F;31-267/Product: trypsin #status predicted <MAT>
F;74,121,224/Domain: trypsin homology <TRY>
F;74,121,224/Active site: His, Asp, Ser #status predicted

Query Match 28.5%; Score 511; DB 2; Length 275;
Best Local Similarity 40.6%; Pred. No. 4.2e-38;
Matches 116; Conservative 40; Mismatches 98; Indels 32; Gaps 11;
QY 22 LALLARAGURKESQEAAPLSPGGRVITSRIVGDEALGRWPQGSRLRL----WDS 77
DB 5 LVIALALLGLSLVPS-----PAPGALQRV---GIVGGEAPGSKWQVSLRKLKQYV-R 56
QY 78 HVGCVSLSHRWALTAACFETYSDLSQSGMVQFQGLTSMPSFWSLQAYTRYF--VS 135
DB 57 HICGSLIHPQWVLTAAHC--VQPNVVCVEIRVQURE-----QHLTYQDHLPLVN 105
QY 136 NYLSPR-PLGNSPYIALVKLSAPVYTKHIQICLOASTFEFENRTDCWVTGWYIKE 194
DB 106 RIVMHPNYPNGADIALLEEDPVNSAHPQVTLFPALQTFPTGTCWVTGWDVHS 165
QY 195 DEALPSPHTIQEYQVAINNSMCN---HLFLKYSFR-KDIFGDMVCAGNAGCGKACFDG 250
DB 166 GTLEPPFPPLKQVKVPIVENSMDVQVHLGLSLTGDGVRIVREDMLCAGNSK--SDSCQD 223
QY 251 SGGFLACNKNGLWYQIGVSWGCGRPNRPGVYTNLSHHFEWIK 296

Db 224 SGGPLVCRVGRVWLOAGVVSWMGEGCAQPNRPGIYTRVAYVLDWIHQ 269

RESULT 10

KQRTPL
plasma kallikrein (EC 3.4.21.34) precursor - rat
N;Alternate names: Fletcher factor; kininogenin; serum kallikrein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 18-Jun-1999
C;Accession: A33180; A33320; S06851; I53041; S06852
R;Beaubien, G.; Rosinski-Chupin, I.; Mattei, M.G.; Mbikay, M.; Chretien, M.; Seidah, N.
Biochemistry 30, 1628-1635, 1991
A;Title: Gene structure and chromosomal localization of plasma kallikrein.
A;Reference number: A33180; MUID: 91129236; PMID: 1993180
A;Accession: A33180
A;Molecule type: DNA
A;Residues: 1-638 <BEA>
A;Cross-references: GB:J05315
A;Note: the authors translated the codon GAG for residue 81 as Gln
R;Seidah, N.G.; Ladenheim, R.; Mbikay, M.; Hamelin, J.; Lutfalla, G.; Rougeon, F.; Laz
DNA 8, 563-574, 1989
A;Title: The cDNA structure of rat plasma kallikrein.
A;Reference number: A33320; MUID: 90091743; PMID: 2598771
A;Accession: A33320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-638 <SEI>
A;Cross-references: GB:M30282; NID:G205010; PIDN:AAA41463.1; PID:G205011
A;Note: part of this sequence, including the amino ends of both the heavy and light cha
R;Paquin, J.; Benjannet, S.; Sawyer, N.; Lazure, C.; Chretien, M.; Seidah, N.G.
Biochim. Biophys. Acta 999, 103-110, 1989
A;Title: Rat plasma kallikrein: purification, NH(2)-terminal sequencing and development
A;Reference number: S06851; MUID: 90089457; PMID: 2597701
A;Accession: S06851
A;Molecule type: protein
A;Residues: 20-45;391-413 <PAQ>
R;Seidah, N.G.; Ladenheim, R.; Mbikay, M.; Hamelin, J.; Lutfalla, G.; Rougeon, R.; Laz
DNA Cell Biol. 8, 563-574, 1989
A;Title: The cDNA structure of rat plasma kallikrein.
A;Reference number: I53041
A;Accession: I53041
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-638 <RES>
A;Cross-references: GB:M58590; NID:G206721; PIDN:AAA42069.1; PID:G206722
C;Comment: This protein, synthesized in the liver, circulates as a noncovalent complex
C;Comment: The zymogen is activated by factor XIIIa, which cleaves the molecule into a l
are linked by one or more disulfide bonds.
C;Genetics:
A;Gene: PK
C;Superfamily: coagulation factor XI; trypsin homology
C;Keywords: blood coagulation; duplication; fibrinolysis; glycoprotein; hydrolase; infl
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-390/Product: plasma kallikrein heavy chain #status experimental <MAT1>
F;20-109/Domain: apple repeat <AP1>
F;110-199/Domain: apple repeat <AP2>
F;200-289/Domain: apple repeat <AP3>
F;291-380/Domain: apple repeat <AP4>
F;391-638/Product: plasma kallikrein light chain #status experimental <MAT2>
F;391-621/Domain: trypsin homology <TRY>
F;121-104, 47-77, 51-57, 111-194, 137-166, 141-147, 201-284, 227-256, 231-237, 292-375, 318-347, 32
F;121, 215, 308, 453, 459, 494/Binding site: carbohydrate (asn) (covalent) #status predicted
F;396/Binding site: carbohydrate (asn) (covalent) #status experimental
F;434, 483, 578/Active site: His, Asp, Ser #status predicted

Query Match 28.5%; Score 511; DB 1; Length 638;
Best Local Similarity 37.7%; Pred. No. 1.2e-37;
Matches 100; Conservative 48; Mismatches 95; Indels 22; Gaps 7;
QY 43 SGPCGRVITSRIVGDEALGRWPQGSRLRL---LWDSHVGCVSLSHRWALTAACFCE- 98
DB 380 SSDCTTK-INARIVGGTNSISGEWPQVSLQVKLVSNHMGSGIIGQWILTAACFDG 438

```

QY 99 -TYSLSLSPSGMVGQGLTSMPSFWSLQAYTRYFVSNIVLSRY-ILGNSPYDIALVKL 156
Db 439 IPYDPVWRIYGIILNLSITNKTFPS-----IKELIHHQYKMSSEGSYDIALIKL 489
QY 157 SAPVYTYKHIPICLQAGSTFFENRTDCWVTGWGVIKEDALPSPHTLQEVQVAILNNSM 216
Db 490 QTELNYTEFFQKICLPSKADNTIYTNVCTGWGTYKERG--EQNILOKATILPVNEE 547
QY 217 CNHLEKYSFRKIDFGDVMVCGAAGGKDAFCGDSGGPLACNKGKLYQIGVSWGVGCG 276
Db 548 CQKYRDYVITK-----OMICAGYKEGGIDACKGDSGGPLVCKGSRWOLVGTISWGRGCA 603
QY 277 RPNRPGVYTNSSHPEWIKLMAQS 301
Db 604 RKEQGVYTKVAEYIDWILEKIQSS 628

RESULT 11
A47246
C:Species: Mus musculus (house mouse)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C:Accession: A47246
R:McNeill, H.P.; Reynolds, D.S.; Schiller, V.; Gildyal, N.; Gurley, D.S.; Austen, K.F.;
Proc. Natl. Acad. Sci. U.S.A. 89, 11174-11178, 1992
A:Title: Isolation, characterization, and transcription of the gene encoding mouse mast
A:Reference number: A47246; MUID:93087489; PMID:1454796
A:Accession: A47246
A>Status: Preliminary
A:Molecule type: nucleic acid
A:Residues: 1-273 <MCN>
A:Cross-references: GB:L00653; NID:g200518; PID:AAA39992.1; PID:g200519
A>Note: sequence extracted from NCBI backbone (NCBIN:119745, NCBI:P:119746)
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine proteinase
F:29-265/Domain: trypsin homology <TRY>

Query Match 28.3%; Score 507; DB 2; Length 273;
Best Local Similarity 42.4%; Pred. No. 9.6e-38;
Matches 114; Conservative 34; Mismatches 87; Indels 34; Gaps 9;

QY 39 AAPLSGCGRRVITSRIYVGGDEALGRWPWGSLRLWDS----HVCVGLSLSHRWALTAH 95
Db 18 AAP--GPANTR---EGIVGGQEAHGNKWPQVSLRANDTYMHFCGSLTHPQWVLTAAH 72
QY 96 CFETYSLSPSGMVGQGLTSMPSFWSLQAYTRYF-----VSNIVLSR-ILGNSPY 149
Db 73 C--VGPDVADENKVRVQ-----LRKQLYVYHDLMTVSQIITHPDFVIQDGA 118
QY 150 DIALVKLSAPVYTYKHIPICLQAGSTFFENRTDCWVTGWGVIKEDALPSPHTLQEVQV 209
Db 119 DIALKLTNPVNI SDYHFEVLPFPASETFPSGTLCTWGTGMDNGVNLNPPFPPLKEVQV 178
QY 210 AIINNSMCHLFLKYSFRKD---IFGDMVCAGNAQGGKDAFCGDSGGPLACNKGKLYQ 265
Db 179 PIENHLCDLYKHKLITGDNVHIVRDDMLCAGNE--GHDSQCGDSGGPLVCKVEDTLQ 236
QY 266 IGWVSWGVGCGRRNRPVYTNISHHFEWI 294
Db 237 AGVSWSGRGCAQPNRPVYTRVTVYLDWI 265

RESULT 12
A45754
C:Species: Homo sapiens (human)
C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 08-Sep-1997
C:Accession: A45754; B37193
R:Miller, J.S.; Westin, E.H.; Schwartz, L.B.
J. Clin. Invest. 84, 1188-1195, 1989
A:Title: Cloning and characterization of complementary DNA for human trypsinase.
A:Reference number: A45754; MUID:90009311; PMID:2677049
A:Accession: A45754

```

```

A:Molecule type: mRNA
A:Residues: 1-274 <MIL>
A:Cross-references: GB:M30038
R:Miller, J.S.; Moxley, G.; Schwartz, L.B.
J. Clin. Invest. 86, 864-870, 1990
A:Title: Cloning and characterization of a second complementary DNA for human trypsinase.
A:Reference number: A37193; MUID:90369005; PMID:2203827
A:Accession: B37193
A:Molecule type: mRNA
A:Residues: 1-274 <MI2>
A:Cross-references: GB:M30038
A>Note: the sequence from Fig. 4 is inconsistent with that from Fig. 2 in having 205-P;
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine proteinase; zymogen
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-30/Domain: activation peptide #status predicted <ACT>
F:31-274/Product: trypsinase I #status predicted <MAT>
F:31-266/Domain: trypsin homology <TRY>
F:74,120,223/Active site: His, Asp, Ser #status predicted

Query Match 28.1%; Score 503.5; DB 2; Length 274;
Best Local Similarity 39.2%; Pred. No. 2e-37;
Matches 112; Conservative 43; Mismatches 96; Indels 35; Gaps 9;

QY 20 LLLAL-LLARAGLRKPESQERAPLSPGCGRRVITSRIYVGGDEALGRWPWGSLRLWD-- 76
Db 5 LLLALPVLASRAYAAPVQALQQAG-----IVGGQEARPKRPWQVSLRVRDRY 54
QY 77 -SHVCGVSLSHRWALTAHCFETYSDISDPGMMVQGLTSMPSFWSLQAYTRYF-- 133
Db 55 WMHFCGSLTHPQWVLTAAHCLG--PDVKDLATLRVNSG-----THLYYQDQLLP 102
QY 134 VSNIVLSR-ILGNSPYDIALVKLSAPVYTYKHIPICLQAGSTFFENRTDCWVTGWGVI 192
Db 103 VSRIMVHPQFYITQIGADIALLEEPVNISSRVHTVMDLPASETFPPGMCPCWVTGWGDV 162
QY 193 KEDEALPSPHTLQEVQVAIINNSMCHLFLKYSFRKD----IFGDMVCAGNAQGGKDAFC 248
Db 163 DNDEPLPFPPLKQVKVPMENHICDAKYHLGAYTGDDVRIIRDDMLCAGNSQ--RDSCK 220
QY 249 GDSGGPLACNKGKLYQIGVSWGVGCGRRNRPVYTNISHHFEWI 294
Db 221 GDSGGPLVCKVNGTQLQAGVSWDSEGCQPNRPVYTRVTVYLDWI 266

RESULT 13
JC4171
C:Species: Rattus norvegicus (Norway rat)
C:Date: 27-Aug-1995 #sequence_revision 27-Oct-1995 #text_change 20-Jun-2000
C:Accession: JC4171
R:Ide, H.; Itoh, H.; Tcmits, M.; Murakumo, Y.; Kobayashi, T.; Matuyama, H.; Osada, Y.;
J. Biochem. 118, 210-215, 1995
A:Title: CDNA sequencing and expression of rat mast cell trypsinase.
A:Reference number: JC4171; MUID:96015171; PMID:8537314
A:Accession: JC4171
A:Molecule type: mRNA
A:Residues: 1-274 <IDE>
A:Cross-references: DDBJ:D38455; NID:g556555; PIDN:BAA07486.1; PID:g556556
C:Comment: This enzyme is basically specific for a connective tissue mast cell, it is a
enzyme inhibitors.
C:Superfamily: trypsin; trypsin homology
C:Keywords: glycoprotein; hydrolase; mast cell; serine proteinase; zymogen
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-29/Domain: activation peptide #status predicted <ACT>
F:30-274/Product: mast cell trypsinase #status predicted <MAT>
F:30-266/Domain: trypsin homology <TRY>
F:73,120,223/Active site: His, Asp, Ser #status predicted
F:31/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 27.9%; Score 500; DB 2; Length 274;
Best Local Similarity 39.3%; Pred. No. 4.1e-37;

```

Matches 116; Conservative 39; Mismatches 102; Indels 38; Gaps 11;

QY 20 LLALLARAGLRKPESQAPLPGCGRRVITRIVGDEAELGRWFWQGSRL-----LW 75
 Db 2 LKLLLLLLLSP--ASLVHAAPC--PVQRV---GIVGREAESKFWQVSLRKFESFW 54
 QY 76 DSHVCGVLLSHRWALTAHCFEYSDLSDPGMMVQFGLTSPFWSLQAYTRY--- 132
 Db 55 -MHFCGGLIHFWQVLTAAHCVGLH--IKSPFLRVQ-----LREQVLYYADQ 99
 QY 133 --FVSNILSPRYLG-NSFYDIALVKLSAPVYTKHQIFICLOASTFEFENRTDCWYTG 189
 Db 100 LLTVNRVTVVHYHYTVEDGADIALLELEIPVNVSTHIFISLPASSTFPGTSCWYTG 159
 QY 190 GYIKEDALPSPHTLOEVOVAIINNSMCNHLFLKYSFRKD-----IFGDMVCAGNAQGGK 245
 Db 160 GDIDSEDELLFPYPLKQVKVPIVENSCLDRKYHTGLYTGDDVPVQDGMLCAGNTR--SD 217
 QY 246 ACFGDSGGFLACNKNGLWYQGVVSWGVGCGRRPGRVYTNISHHFEWIKLMAQ 300
 Db 218 SCQDSGGFLCKVKGWGLQAGVSWGEGCAENRPGIYTRYVYLDWIHYVPQ 272

RESULT 14
 KFHUI
 coagulation factor Xia (EC 3.4.21.27) precursor [validated] - human
 N:Alternate names: antihemophilic factor C; plasma thromboplastin antecedent
 C:Species: Homo sapiens (man)
 C:Date: 13-Aug-1986 #sequence_revision 26-May-1994 #text_change 08-Dec-2000
 C:Accession: A27431; A00920; A37940
 R:Asakai, R.; Davie, E.W.; Chung, D.W.
 Biochemistry 26, 7221-7228, 1987
 A:Title: Organization of the gene for human factor XI.
 A:Reference number: A27431; MUID:88107663; PMID:2827746
 A:Accession: A27431
 A:Molecule type: DNA
 A:Residues: 1-625 <ASA>
 A:Cross-references: GB:M18295
 A>Note: the sequence shown follows the authors' translation
 R:Fujikawa, K.; Chung, D.W.; Hendrickson, L.E.; Davie, E.W.
 Biochemistry 25, 2417-2424, 1986
 A:Title: Amino acid sequence of human factor XI, a blood coagulation factor with four tyrosine residues.
 A:Reference number: A00920; MUID:86243360; PMID:3636155
 A:Accession: A00920
 A:Molecule type: protein
 A:Residues: 1-625 <FU>
 A:Cross-references: GB:M13142; NID:g182832; PIDN:AAA52487.1; PID:g182833
 R:McMullen, B.A.; Fujikawa, K.; Davie, E.W.
 Biochemistry 30, 2056-2060, 1991
 A:Title: Location of the disulfide bonds in human coagulation factor XI: the presence of two intrachain and one interchain disulfide bonds.
 A:Reference number: A37940; MUID:91152017; PMID:1998667
 A:Accession: A37940
 A:Molecule type: protein
 A:Residues: 28-33;35-49, 'X', 51-55, 'X', 57-63;70-75, 'X', 77-79;107-109, 'X', 111-112;132-139, 'X', 141-142;144-145, 'X', 147-148;150-151, 'X', 153-154;156-157, 'X', 159-160;162-163, 'X', 165-166;168-169, 'X', 171-172;174-175, 'X', 177-178;180-181, 'X', 183-184;186-187, 'X', 189-190;192-193, 'X', 195-196;198-199, 'X', 201-202;204-205, 'X', 207-208;210-211, 'X', 213-214;216-217, 'X', 219-220;222-223, 'X', 225-226;228-229, 'X', 231-232;234-235, 'X', 237-238;240-241, 'X', 243-244;246-247, 'X', 249-250;252-253, 'X', 255-256;258-259, 'X', 261-262;264-265, 'X', 267-268;270-271, 'X', 273-274;276-277, 'X', 279-280;282-283, 'X', 285-286;288-289, 'X', 291-292;294-295, 'X', 297-298;300-301, 'X', 303-304;306-307, 'X', 309-310;312-313, 'X', 315-316;318-319;320-326, 'X', 328-330;332-333, 'X', 335-336;338-339;340-341, 'X', 343-344;346-347, 'X', 349-350;352-353, 'X', 355-356;358-359, 'X', 361-362;364-365, 'X', 367-368;370-371, 'X', 373-374;376-377, 'X', 379-380;382-383, 'X', 385-386;388-389, 'X', 391-392;394-395, 'X', 397-398;399-400, 'X', 403-404;406-407, 'X', 409-410;412-413, 'X', 415-416;418-419, 'X', 421-422;424-425, 'X', 427-428;430-431, 'X', 433-434;436-437, 'X', 439-440;442-443, 'X', 445-446;448-449, 'X', 451-452;454-455, 'X', 457-458;460-461, 'X', 463-464;466-467, 'X', 469-470;472-473, 'X', 475-476;478-479, 'X', 481-482;484-485, 'X', 487-488;490-491, 'X', 493-494;496-497, 'X', 499-500;502-503, 'X', 505-506;508-509, 'X', 511-512;514-515, 'X', 517-518;520-521, 'X', 523-524;526-527, 'X', 529-530;532-533, 'X', 535-536;538-539, 'X', 541-542;544-545, 'X', 547-548;550-551, 'X', 553-554;556-557, 'X', 559-560;562-563, 'X', 565-566;568-569, 'X', 571-572;574-575, 'X', 577-578;580-581, 'X', 583-584;586-587, 'X', 589-590;592-593, 'X', 595-596;598-599, 'X', 601-602;604-605, 'X', 607-608;610-611, 'X', 613-614;616-617, 'X', 619-620;622-623, 'X', 625-626;628-629, 'X', 631-632;634-635, 'X', 637-638;640-641, 'X', 643-644;646-647, 'X', 649-650;652-653, 'X', 655-656;658-659, 'X', 661-662;664-665, 'X', 667-668;670-671, 'X', 673-674;676-677, 'X', 679-680;682-683, 'X', 685-686;688-689, 'X', 691-692;694-695, 'X', 697-698;699-700, 'X', 703-704;706-707, 'X', 709-710;712-713, 'X', 715-716;718-719, 'X', 721-722;724-725, 'X', 727-728;730-731, 'X', 733-734;736-737, 'X', 739-740;742-743, 'X', 745-746;748-749, 'X', 751-752;754-755, 'X', 757-758;760-761, 'X', 763-764;766-767, 'X', 769-770;772-773, 'X', 775-776;778-779, 'X', 781-782;784-785, 'X', 787-788;790-791, 'X', 793-794;796-797, 'X', 799-800;802-803, 'X', 805-806;808-809, 'X', 811-812;814-815, 'X', 817-818;820-821, 'X', 823-824;826-827, 'X', 829-830;832-833, 'X', 835-836;838-839, 'X', 841-842;844-845, 'X', 847-848;850-851, 'X', 853-854;856-857, 'X', 859-860;862-863, 'X', 865-866;868-869, 'X', 871-872;874-875, 'X', 877-878;880-881, 'X', 883-884;886-887, 'X', 889-890;892-893, 'X', 895-896;898-899, 'X', 901-902;904-905, 'X', 907-908;910-911, 'X', 913-914;916-917, 'X', 919-920;922-923, 'X', 925-926;928-929, 'X', 931-932;934-935, 'X', 937-938;940-941, 'X', 943-944;946-947, 'X', 949-950;952-953, 'X', 955-956;958-959, 'X', 961-962;964-965, 'X', 967-968;970-971, 'X', 973-974;976-977, 'X', 979-980;982-983, 'X', 985-986;988-989, 'X', 991-992;994-995, 'X', 997-998;999-1000, 'X', 1003-1004;1006-1007, 'X', 1009-1010;1012-1013, 'X', 1015-1016;1018-1019, 'X', 1021-1022;1024-1025, 'X', 1027-1028;1030-1031, 'X', 1033-1034;1036-1037, 'X', 1039-1040;1042-1043, 'X', 1045-1046;1048-1049, 'X', 1051-1052;1054-1055, 'X', 1057-1058;1060-1061, 'X', 1063-1064;1066-1067, 'X', 1069-1070;1072-1073, 'X', 1075-1076;1078-1079, 'X', 1081-1082;1084-1085, 'X', 1087-1088;1090-1091, 'X', 1093-1094;1096-1097, 'X', 1099-1100;1102-1103, 'X', 1105-1106;1108-1109, 'X', 1111-1112;1114-1115, 'X', 1117-1118;1120-1121, 'X', 1123-1124;1126-1127, 'X', 1129-1130;1132-1133, 'X', 1135-1136;1138-1139, 'X', 1141-1142;1144-1145, 'X', 1147-1148;1150-1151, 'X', 1153-1154;1156-1157, 'X', 1159-1160;1162-1163, 'X', 1165-1166;1168-1169, 'X', 1171-1172;1174-1175, 'X', 1177-1178;1180-1181, 'X', 1183-1184;1186-1187, 'X', 1189-1190;1192-1193, 'X', 1195-1196;1198-1199, 'X', 1201-1202;1204-1205, 'X', 1207-1208;1210-1211, 'X', 1213-1214;1216-1217, 'X', 1219-1220;1222-1223, 'X', 1225-1226;1228-1229, 'X', 1231-1232;1234-1235, 'X', 1237-1238;1240-1241, 'X', 1243-1244;1246-1247, 'X', 1249-1250;1252-1253, 'X', 1255-1256;1258-1259, 'X', 1261-1262;1264-1265, 'X', 1267-1268;1270-1271, 'X', 1273-1274;1276-1277, 'X', 1279-1280;1282-1283, 'X', 1285-1286;1288-1289, 'X', 1291-1292;1294-1295, 'X', 1297-1298;1300-1301, 'X', 1303-1304;1306-1307, 'X', 1309-1310;1312-1313, 'X', 1315-1316;1318-1319, 'X', 1321-1322;1324-1325, 'X', 1327-1328;1330-1331, 'X', 1333-1334;1336-1337, 'X', 1339-1340;1342-1343, 'X', 1345-1346;1348-1349, 'X', 1351-1352;1354-1355, 'X', 1357-1358;1360-1361, 'X', 1363-1364;1366-1367, 'X', 1369-1370;1372-1373, 'X', 1375-1376;1378-1379, 'X', 1381-1382;1384-1385, 'X', 1387-1388;1390-1391, 'X', 1393-1394;1396-1397, 'X', 1399-1400;1402-1403, 'X', 1405-1406;1408-1409, 'X', 1411-1412;1414-1415, 'X', 1417-1418;1420-1421, 'X', 1423-1424;1426-1427, 'X', 1429-1430;1432-1433, 'X', 1435-1436;1438-1439, 'X', 1441-1442;1444-1445, 'X', 1447-1448;1450-1451, 'X', 1453-1454;1456-1457, 'X', 1459-1460;1462-1463, 'X', 1465-1466;1468-1469, 'X', 1471-1472;1474-1475, 'X', 1477-1478;1480-1481, 'X', 1483-1484;1486-1487, 'X', 1489-1490;1492-1493, 'X', 1495-1496;1498-1499, 'X', 1501-1502;1504-1505, 'X', 1507-1508;1510-1511, 'X', 1513-1514;1516-1517, 'X', 1519-1520;1522-1523, 'X', 1525-1526;1528-1529, 'X', 1531-1532;1534-1535, 'X', 1537-1538;1540-1541, 'X', 1543-1544;1546-1547, 'X', 1549-1550;1552-1553, 'X', 1555-1556;1558-1559, 'X', 1561-1562;1564-1565, 'X', 1567-1568;1570-1571, 'X', 1573-1574;1576-1577, 'X', 1579-1580;1582-1583, 'X', 1585-1586;1588-1589, 'X', 1591-1592;1594-1595, 'X', 1597-1598;1599-1600, 'X', 1603-1604;1606-1607, 'X', 1609-1610;1612-1613, 'X', 1615-1616;1618-1619, 'X', 1621-1622;1624-1625, 'X', 1627-1628;1630-1631, 'X', 1633-1634;1636-1637, 'X', 1639-1640;1642-1643, 'X', 1645-1646;1648-1649, 'X', 1651-1652;1654-1655, 'X', 1657-1658;1660-1661, 'X', 1663-1664;1666-1667, 'X', 1669-1670;1672-1673, 'X', 1675-1676;1678-1679, 'X', 1681-1682;1684-1685, 'X', 1687-1688;1690-1691, 'X', 1693-1694;1696-1697, 'X', 1699-1700;1702-1703, 'X', 1705-1706;1708-1709, 'X', 1711-1712;1714-1715, 'X', 1717-1718;1720-1721, 'X', 1723-1724;1726-1727, 'X', 1729-1730;1732-1733, 'X', 1735-1736;1738-1739, 'X', 1741-1742;1744-1745, 'X', 1747-1748;1750-1751, 'X', 1753-1754;1756-1757, 'X', 1759-1760;1762-1763, 'X', 1765-1766;1768-1769, 'X', 1771-1772;1774-1775, 'X', 1777-1778;1780-1781, 'X', 1783-1784;1786-1787, 'X', 1789-1790;1792-1793, 'X', 1795-1796;1798-1799, 'X', 1801-1802;1804-1805, 'X', 1807-1808;1810-1811, 'X', 1813-1814;1816-1817, 'X', 1819-1820;1822-1823, 'X', 1825-1826;1828-1829, 'X', 1831-1832;1834-1835, 'X', 1837-1838;1840-1841, 'X', 1843-1844;1846-1847, 'X', 1849-1850;1852-1853, 'X', 1855-1856;1858-1859, 'X', 1861-1862;1864-1865, 'X', 1867-1868;1870-1871, 'X', 1873-1874;1876-1877, 'X', 1879-1880;1882-1883, 'X', 1885-1886;1888-1889, 'X', 1891-1892;1894-1895, 'X', 1897-1898;1899-1900, 'X', 1903-1904;1906-1907, 'X', 1909-1910;1912-1913, 'X', 1915-1916;1918-1919, 'X', 1921-1922;1924-1925, 'X', 1927-1928;1930-1931, 'X', 1933-1934;1936-1937, 'X', 1939-1940;1942-1943, 'X', 1945-1946;1948-1949, 'X', 1951-1952;1954-1955, 'X', 1957-1958;1959-1960, 'X', 1963-1964;1966-1967, 'X', 1969-1970;1972-1973, 'X', 1975-1976;1978-1979, 'X', 1981-1982;1984-1985, 'X', 1987-1988;1989-1990, 'X', 1993-1994;1996-1997, 'X', 1999-2000;2002-2003, 'X', 2005-2006;2008-2009, 'X', 2011-2012;2014-2015, 'X', 2017-2018;2020-2021, 'X', 2023-2024;2026-2027, 'X', 2029-2030;2032-2033, 'X', 2035-2036;2038-2039, 'X', 2041-2042;2044-2045, 'X', 2047-2048;2050-2051, 'X', 2053-2054;2056-2057, 'X', 2059-2060;2062-2063, 'X', 2065-2066;2068-2069, 'X', 2071-2072;2074-2075, 'X', 2077-2078;2080-2081, 'X', 2083-2084;2086-2087, 'X', 2089-2090;2092-2093, 'X', 2095-2096;2098-2099, 'X', 2101-2102;2104-2105, 'X', 2107-2108;2110-2111, 'X', 2113-2114;2116-2117, 'X', 2119-2120;2122-2123, 'X', 2125-2126;2128-2129, 'X', 2131-2132;2134-2135, 'X', 2137-2138;2140-2141, 'X', 2143-2144;2146-2147, 'X', 2149-2150;2152-2153, 'X', 2155-2156;2158-2159, 'X', 2161-2162;2164-2165, 'X', 2167-2168;2170-2171, 'X', 2173-2174;2176-2177, 'X', 2179-2180;2182-2183, 'X', 2185-2186;2188-2189, 'X', 2191-2192;2194-2195, 'X', 2197-2198;2199-2200, 'X', 2203-2204;2206-2207, 'X', 2209-2210;2212-2213, 'X', 2215-2216;2218-2219, 'X', 2221-2222;2224-2225, 'X', 2227-2228;2230-2231, 'X', 2233-2234;2236-2237, 'X', 2239-2240;2242-2243, 'X', 2245-2246;2248-2249, 'X', 2251-2252;2254-2255, 'X', 2257-2258;2260-2261, 'X', 2263-2264;2266-2267, 'X', 2269-2270;2272-2273, 'X', 2275-2276;2278-2279, 'X', 2281-2282;2284-2285, 'X', 2287-2288;2290-2291, 'X', 2293-2294;2296-2297, 'X', 2299-2300;2302-2303, 'X', 2305-2306;2308-2309, 'X', 2311-2312;2314-2315, 'X', 2317-2318;2320-2321, 'X', 2323-2324;2326-2327, 'X', 2329-2330;2332-2333, 'X', 2335-2336;2338-2339, 'X', 2341-2342;2344-2345, 'X', 2347-2348;2350-2351, 'X', 2353-2354;2356-2357, 'X', 2359-2360;2362-2363, 'X', 2365-2366;2368-2369, 'X', 2371-2372;2374-2375, 'X', 2377-2378;2380-2381, 'X', 2383-2384;2386-2387, 'X', 2389-2390;2392-2393, 'X', 2395-2396;2398-2399, 'X', 2401-2402;2404-2405, 'X', 2407-2408;2410-2411, 'X', 2413-2414;2416-2417, 'X', 2419-2420;2422-2423, 'X', 2425-2426;2428-2429, 'X', 2431-2432;2434-2435, 'X', 2437-2438;2440-2441, 'X', 2443-2444;2446-2447, 'X', 2449-2450;2452-2453, 'X', 2455-2456;2458-2459, 'X', 2461-2462;2464-2465, 'X', 2467-2468;2470-2471, 'X', 2473-2474;2476-2477, 'X', 2479-2480;2482-2483, 'X', 2485-2486;2488-2489, 'X', 2491-2492;2494-2495, 'X', 2497-2498;2499-2500, 'X', 2503-2504;2506-2507, 'X', 2509-2510;2512-2513, 'X', 2515-2516;2518-2519, 'X', 2521-2522;2524-2525, 'X', 2527-2528;2530-2531, 'X', 2533-2534;2536-2537, 'X', 2539-2540;2542-2543, 'X', 2545-2546;2548-2549, 'X', 2551-2552;2554-2555, 'X', 2557-2558;2560-2561, 'X', 2563-2564;2566-2567, 'X', 2569-2570;2572-2573, 'X', 2575-2576;2578-2579, 'X', 2581-2582;2584-2585, 'X', 2587-2588;2589-2590, 'X', 2593-2594;2596-2597, 'X', 2599-2600;2602-2603, 'X', 2605-2606;2608-2609, 'X', 2611-2612;2614-2615, 'X', 2617-2618;2620-2621, 'X', 2623-2624;2626-2627, 'X', 2629-2630;2632-2633, 'X', 2635-2636;2638-2639, 'X', 2641-2642;2644-2645, 'X', 2647-2648;2650-2651, 'X', 2653-2654;2656-2657, 'X', 2659-2660;2662-2663, 'X', 2665-2666;2668-2669, 'X', 2671-2672;2674-2675, 'X', 2677-2678;2680-2681, 'X', 2683-2684;2686-2687, 'X', 2689-2690;2692-2693, 'X', 2695-2696;2698-2699, 'X', 2701-2702;2704-2705, 'X', 2707-2708;2710-2711, 'X', 2713-2714;2716-2717, 'X', 2719-2720;2722-2723, 'X', 2725-2726;2728-2729, 'X', 2731-2732;2734-2735, 'X', 2737-2738;2740-2741, 'X', 2743-2744;2746-2747, 'X', 2749-2750;2752-2753, 'X', 2755-2756;2758-2759, 'X', 2761-2762;2764-2765, 'X', 2767-2768;2770-2771, 'X', 2773-2774;2776-2777, 'X', 2779-2780;2782-2783, 'X', 2785-2786;2788-2789, 'X', 2791-2792;2794-2795, 'X', 2797-2798;2799-2800, 'X', 2803-2804;2806-2807, 'X', 2809-2810;2812-2813, 'X', 2815-2816;2818-2819, 'X', 2821-2822;2824-2825, 'X', 2827-2828;2830-2831, 'X', 2833-2834;2836-2837, 'X', 2839-2840;2842-2843, 'X', 2845-2846;2848-2849, 'X', 2851-2852;2854-2855, 'X', 2857-2858;2860-2861, 'X', 2863-2864;2866-2867, 'X', 2869-2870;2872-2873, 'X', 2875-2876;2878-2879, 'X', 2881-2882;2884-2885, 'X', 2887-2888;2889-2890, 'X', 2893-2894;2896-2897, 'X', 2899-2900;2902-2903, 'X', 2905-2906;2908-2909, 'X', 2911-2912;2914-2915, 'X', 2917-2918;2920-2921, 'X', 2923-2924;2926-2927, 'X', 2929-2930;2932-2933, 'X', 2935-2936;2938-2939, 'X', 2941-2942;2944-2945, 'X', 2947-2948;2950-2951, 'X', 2953-2954;2956-2957, 'X', 2959-2960;2962-2963, 'X', 2965-2966;2968-2969, 'X', 2971-2972;2974-2975, 'X', 2977-2978;2979-2980, 'X', 2983-2984;2986-2987, 'X', 2989-2990;2992-2993, 'X', 2995-2996;2998-2999, 'X', 3001-3002;3004-3005, 'X', 3007-3008;3010-3011, 'X', 3013-3014;3016-3017, 'X', 3019-3020;3022-3023, 'X', 3025-3026;3028

Search completed: April 6, 2004, 14:13:37
Job time : 21 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2004, 14:09:09 ; Search time 45 Seconds
(without alignments)
2292.766 Million cell updates/sec

Title: US-09-787-844-2
Perfect score: 1792
Sequence: 1 RQRGRQAGEAMGARGAL.....PSWPLLPFLWALPLGPV 327

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- SPTREMBL 25:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_rhco:*
 - 8: sp_organelle:*
 - 9: sp_phase:*
 - 10: sp_plant:*
 - 11: sp_protent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriap:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1178	65.7	336	11 Q80YD8	Q80YD8 mus musculus
2	1123.5	62.7	328	11 Q80Z40	Q80Z40 rattus norv
3	845	47.2	322	11 Q920S2	Q920S2 mus musculus
4	812	45.3	282	11 Q9P4I3	Q944i3 mus musculus
5	602	33.6	321	4 Q96RZ8	Q96RZ8 homo sapien
6	580.5	32.4	389	13 Q9PVX7	Q9PVX7 xenopus lae
7	580	32.4	328	11 Q8BJR6	Q8BJR6 mus musculus
8	572.5	31.9	311	11 Q80XZ3	Q80XZ3 rattus norv
9	571.5	31.9	331	11 Q8R1A6	Q8R1A6 mus musculus
10	568.5	31.7	331	11 Q80X17	Q80X17 mus musculus
11	565.5	31.6	339	11 Q9ZL44	Q9ZL44 mus musculus
12	561	31.3	337	13 Q9DGR3	Q9DGR3 xenopus lae
13	550	30.7	340	11 Q8BJV6	Q8BJV6 mus musculus
14	534.5	29.8	307	11 Q7TML0	Q7TML0 mus musculus
15	533.5	29.8	297	11 Q88781	Q88781 rattus ratt
16	532.5	29.7	310	11 Q91XC4	Q91XC4 mus musculus

17	524.5	29.3	310	11 Q9QYZ9	Q9QYZ9 mus musculus
18	522.5	29.2	471	11 Q8CFE0	Q8CFE0 mus musculus
19	522	29.1	273	6 Q9XSM1	Q9XSM1 ovis aries
20	516.5	28.8	558	4 Q86YM4	Q86YM4 homo sapien
21	515.5	28.8	581	4 Q9BYE2	Q9BYE2 homo sapien
22	515	28.7	275	4 Q96RZ6	Q96RZ6 homo sapien
23	512.5	28.6	537	4 Q9BYE1	Q9BYE1 homo sapien
24	512	28.6	417	11 Q8BZ10	Q8BZ10 mus musculus
25	511.5	28.5	257	11 Q8BZ04	Q8BZ04 mus musculus
26	511	28.5	320	13 Q7T0X2	Q7T0X2 xenopus lae
27	510	28.5	643	6 Q97506	Q97506 sus scrofa
28	509	28.4	273	11 Q921N4	Q921N4 mus musculus
29	508.5	28.4	638	11 Q8R0P5	Q8R0P5 mus musculus
30	506	28.2	277	11 Q80WM7	Q80WM7 mus musculus
31	506	28.2	453	11 Q81ZAG	Q81ZAG mus musculus
32	504	28.1	624	11 Q9DAT3	Q9DAT3 mus musculus
33	502	28.0	624	11 Q91Y47	Q91Y47 mus musculus
34	501	28.0	275	4 Q86TM8	Q86TM8 homo sapien
35	501	28.0	276	4 Q86UA5	Q86UA5 homo sapien
36	500.5	27.9	767	13 Q9DGR2	Q9DGR2 xenopus lae
37	497.5	27.8	327	4 Q8N171	Q8N171 homo sapien
38	496.5	27.7	284	4 Q8NF86	Q8NF86 homo sapien
39	496.5	27.7	329	13 Q42Z72	Q42Z72 xenopus lae
40	493.5	27.5	371	11 Q8CJ16	Q8CJ16 rattus norv
41	493.5	27.5	445	11 Q8CJ17	Q8CJ17 rattus norv
42	491	27.4	271	6 Q8HXJ2	Q8HXJ2 bos taurus
43	489.5	27.3	293	4 Q7Z5A4	Q7Z5A4 homo sapien
44	486.5	27.1	455	11 Q8CDR0	Q8CDR0 mus musculus
45	486	27.1	855	4 Q7Z410	Q7Z410 homo sapien

ALIGNMENTS

RESULT 1

Q80YD8	PRELIMINARY;	PRT;	336 AA.
ID Q80YD8;			
AC Q80YD8;			
DT 01-JUN-2003 (TREMBlrel. 24, Created)			
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)			
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)			
DE Similar to protease, serine, 21 (Fragment).			
OS Mus musculus (Mouse).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX NCBI_taxID=10090;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC TISSUE=Testicle;			
RA Strauberg R.;			
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.			
DR EMBL; BC049588; AAH49588.1; .			
DR GO; GO:0004263; F:chymotrypsin activity; IEA.			
DR GO; GO:0008233; F:peptidase activity; IEA.			
DR GO; GO:0004235; F:trypsin activity; IEA.			
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.			
DR InterPro; IPR009003; Cys_Ser_trypsin.			
DR InterPro; IPR001254; Peptidase_S1.			
DR Pfam; PF00089; trypsin; 1.			
DR PRINTS; PR00722; CHYMOTRYPSIN.			
DR SMART; SM00020; Tryp_Src; 1.			
DR PROSITE; PS00240; TRYPSIN_DOM; 1.			
DR PROSITE; PS00134; TRYPSIN_HIS; 1.			
DR PROSITE; PS00135; TRYPSIN_SER; 1.			
KW Protease.			
FT NON TER			
SQ SEQUENCE 336 AA; 37361 MW; E5206FEDBE55C670 CRC64;			

Query Match 65.7%; Score 1178; DB 11; Length 336;
Best Local Similarity 64.7%; Pred.No. 1.6e-101;
Matches 218; Conservative 40; Mismatches 63; Indels 16; Gaps 4;

```

QY 3 QGRQAGEAMGARGALLALL--LABAGL-----RKPEQCEAAPLSGCGRR 49
Db 2 KGCQVAGEVANGARGKTLVPLVLLVATAAALOSTYLOVDPEKPELDLLSGCGHR 61
QY 50 VITSRIVGGEDEAELGRWQWQSRLRWDSHVCGVSLLSHRMALTAAHCFETYSDLSPSGW 109
Db 62 TIPSRIVGDDAELGRWQWQSRLRWGNHLGATLLNRRWYLTAAHCFQ--KD-NDPFDW 118
QY 110 MVQFQOLSMPSFMSLOAYVYTRYFVSNLYLSPRYLGNPSFDIALVKLSABVYTKHQI 169
Db 119 TVQFGLTSRPSLWNLQAYSNRYQEDIFLSPKSEQVNDIALKLUSSVYTNNTQI 178
QY 170 CLQASTFEFENRTDCWVTGWGYIKEDEALPSPHTLQEVQVAIINNSMCHLFLKYSFRK 229
Db 179 CLLNSTYKPENRTDCWVTGWAIGADESLSPNTLQEVQVAIINNSMCHMYKKPFRTN 238
QY 230 IFGDMVCAGNAGGKDACFGSGGSLPACNKNGLWQICGVYSGWGCGRPNRPGVYTNISH 289
Db 239 IGDWMVCATPBGKDACFGSGGSLPACQDQTVWQGVVSWGICGRPNRPGVYTNISH 298
QY 290 HFEWIKUNQAQSGMSQDPDSWPLFFJFFLLWALPLGP 326
Db 299 HYNWQSTMRNGLLRPPVPLLLFTLWASSLLRP 335

```

```

QY 182 TDWVTGWGVIKED-EALPSPHTLQEVQVVAIINNMCNHLFLKYSFRKQIFGDMVCAGNA 240
Db 176 PRWVTGWVQLDKLPPLPPYHLREVQVQSILNNSRCQELFEIIFSLHLITDKDVFCAE 235
QY 241 QGKADACFGDSGLPLACNKNGLWYQIGVSWGVCGRNRPVYVTVNISHHFEWIOKLMQA 300
Db 236 DGSADTCSDGSGPLVNCMDGLWYQIGVSWGVCGRNRPVYVTVNISHHFEWIOKLMQA 295
QY 301 SGMSQDPDSWPLIFFPFLWALPLLP 326
Db 296 NGAVRRDLALPILLSITLLQAPWLLRP 321

RESULT 4
Q9D413 PRELIMINARY; PRT; 282 AA.
AC Q9D413
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE 4931440B09Rik protein.
GN 4931440B09Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayaehizaki Y.,
RA "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AK016509; BAB30277.1; -
DR HSSP; P00763; IDPO.
DR MSROPS; S01.417; -.
DR MGD; MGI.1918253; 4931440B09Rik.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF000089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 282 AA; 31997 MW; 48D89B74F750BAB4 CRC64;

Query Match 45.3%; Score 812; DB 11; Length 282;
Best Local Similarity 54.9%; Pred. No. 1.8e-67;

```

```

Matches 156; Conservative 40; Mismatches 82; Indels 6; Gaps 4;
QY 45 PCGRVIT-SRIVGEDAELGRWPQGSRLRWDVSHVCGVSLSHRWALTAHCFETYSDL 103
Db 2 PCGRNDRSRIVGIGISMQRWQASRLRLKSHRCGSLSSRWVLTAAHCFKY--- 58
QY 104 SDPGWVQFQLTSMSPFWSLQAYTRYFVSNIYLSFRLGNSPYDIALVKLSAPVYIT 163
Db 59 LDPEKWTYQLGLTSKPSYNNRKAYSGRYRKDIIVNSEDKLS-HDLALRLASSVYTN 117
QY 164 KHIOPICLQASTFEFNRNDCWVTGWGVIKED-EALPSPHTLQEVQVVAIINNMCNHLFL 222
Db 118 KDQPVCVQSPSTFTSQHPQPCWVTGWVQLQEDLXPLPPYHLREVQVSIINNSRCQELFE 177
QY 223 KYSFRKQIFGDMVCAGNAQGGKDACFGDSGGLPLACNKNGLWYQIGVSWGVCGRNRP 282
Db 178 IFSLHLITDKDVFCAEADGSDATCSGDSGLPLVNCMDGLWYQIGVSWGVCGRNLP 237
QY 283 VYTNISHHFEWIOKLMQAQSGMSQDPDSWPLIFFPFLWALPLLP 326
Db 238 IYTVNISHHFEWIOKLMQAQSGMSQDPDSWPLIFFPFLWALPLLP 281

RESULT 5
Q96RZ8 PRELIMINARY; PRT; 321 AA.
AC Q96RZ8
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE HS transmembrane trypsin, gene name TWT, AF175522.1.
GN TRPA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21095910; PubMed=11157797;
RA Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
RA Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
RA Higgins D.R.;
RA "Sequence, structure and pathology of the fully annotated terminal 2 Mb of the short arm of human chromosome 16.";
RL Hum. Mol. Genet. 10:339-352(2001).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AE006466; AAK61269.1; -
DR HSSP; P00761; IAN1.
DR GO; GO:0001602; C:integral to membrane; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
KW Hydrolase; Protease; Serine protease; Transmembrane.
SQ SEQUENCE 321 AA; 33829 MW; FFF5089EDC4FC73D CRC64;

Query Match 33.6%; Score 602; DB 4; Length 321;
Best Local Similarity 42.9%; Pred. No. 8.5e-48;
Matches 140; Conservative 40; Mismatches 98; Indels 48; Gaps 11;
QY 13 AMGARGALLIALALLARAGLRKPSQEAAPISGPGRRVIT---SRIVGGEDELGRWPQ 69
Db 2 ALGACG-LALLAVFGVSLR-----TLQPGCRFQVSDAGRGVGGHAAPAGWPQ 52
QY 70 GSLRLWDSHVCVGSLLSHRWALTAHCFETYSDLSDPGSMWVQGL--TSMPSFWSLQA 127

```

```

Db 53 ASLRRLRVHVGCGSLSPQWLTAAHCFSGSLNSD---YQVHLGELEITLSPHFSTVRQ 109
QY 128 YTRYFVSNIVLSPRYLGNSPVDIALVKLSAPVTVTKHQICLQASFFENRTDCWWT 187
Db 110 II-----LHSSPSGQGTSCDIALVELSVPTLSSRLFLVCLPEASDFPCGIRCWWT 162
QY 188 GWGYIKEDBALPSPHTLOEVQVAIINNSMCHLFLKYSFRKDFG-----DMVCAGN 239
Db 163 GWGYITREGEPLPPYSLSREVKSVVVDTEC-----RRDYFGGSGILQPMCLC--- 210
QY 240 AQGGKDACFGGSGGLACNKGWLTQIGVSWGCGGNRPVTVTNIHHFVWIKLMA 299
Db 211 ARGPGDACCDDSGGLVCGVNGAWQAGIVSWGCGGNRPVTVTVTPAVVNWIRRHIT 270
QY 300 QSGMSQPD-PSWPLL---FFPLLWAL 321
Db 271 ASGGSESGYPLPLLAGFPLFLGL 296

RESULT 6
Q3PVX7 PRELIMINARY; PRT; 389 AA.
ID AC Q3PVX7;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Epidermis specific serine protease.
GN XEPSIN.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K.;
RT "The expression control of xepsin by non-axial and planar
RT posteriorizing signals in Xenopus epidermis.";
RT Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AB018694; BAA84941.1; --
DR HSSP; P00763; 1DPO.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PRO00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS0240; TRYPsin DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; 1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 389 AA; 42375 MW; B1FBA42F5D1F6E3 CRC64;

Query Match 32.4%; Score 580.5; DB 13; Length 389;
Best Local Similarity 40.2%; Pred. No. 1.1e-45;
Matches 121; Conservative 43; Mismatches 84; Indels 53; Gaps 7;

QY 46 GBRVITRIYGGDAELGRPMQGLSLWDSHVGVGYSLLSHRWALTAACFFETYS----- 101
Db 17 CCVPVISHRIYVGMDSKKGEMFWQISYKSDSCGSLTDSWMTAAHCIDSLDVSYY 76
QY 102 -----DLSDPSGMWVFG--QLTSMPSFWSLQAYTRYFVSNIVLSPRYLGNSPVDIA 152
Db 77 TVVLGAYQLSAPDNTSVSRGVKSIKHPDF-----QYEGSSG-DIA 116
QY 153 LVKLSAPVTVTKHQICLQASFFENRTDCWWTGWYIKEDBALPSPHTLQEVQVAII 212

```

```

Db 117 LIELEKPVTFPIYILPCLPSQDVQFAAGTMCWTVGWNIGBTPLISPKTIQKAEVAII 176
QY 213 NNSMCHNHLFLK-----YSFRKDFGDMVCAGNAGGKDACFGDSGGPLACNKGWLTQ 265
Db 177 DSVCGTMYESSLGVIPDFSFQIE---DMVCAGYKEGRIDACQDGGGGLVCNNVWMLQ 233
QY 266 IGVVSGVCGGPNRPVTVTNIHHFVWIKLMAQSGMSQPDPSWPLLFFPLLWALPLLQ 325
Db 234 LGIVSGYGCAPENRPGVTVTVQYQDWLKTNPVLFSEEGFS-----VAPSIG 283
QY 326 P 326
Db 284 P 284

RESULT 7
Q8BJR6 PRELIMINARY; PRT; 328 AA.
ID AC Q8BJR6;
DT 01-MAR-2003 (TREMELrel. 23, Created)
DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Similar to MARAPsin precursor (Channel-activating protease 2-like
DE protein) (Pancreasin).
GN PEN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The PANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=12986/SvEvTac;
RC Brathwaite M., Waeltz P., Schlessinger D., Nagaraja R.;
RT "Genomic Sequence Analysis in the Mouse T-complex Region.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6; TISSUE=Bladder;
RX MEDLINE=22439795; PubMed=12411343;
RA Bhagwandin V.J., Hau L.W., Mallen-St Clair J., Walters P.J.,
RT Caughey G.H.;
RT "Structure and activity of human pancreasin, a novel tryptic serine
RT peptidase expressed primarily by the pancreas.";
RL J. Biol. Chem. 5:3363-3371(2003).
DR EMBL; AX080281; BAC37864.1; --
DR EMBL; AY162410; AA017162.1; --
DR EMBL; AF542056; AA027572.1; --
DR MGD; MGI:2450323; Mpn.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PRO00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS0240; TRYPsin DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; 1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
KW Protease.
SQ SEQUENCE 328 AA; 35789 MW; DC0B20F1AB3EB840 CRC64;

```

```
Query Match 32.4%; Score 580; DB 11; Length 328;
Best Local Similarity 43.8%; Pred. No. 9.9e-46;
Matches 126; Conservative 42; Mismatches 94; Indels 28; Gaps 8;

QY 19 ALLALLARAGLRKPSQEAAPLSGCGRRVITSRIYGGEDAEALGRWPQGSRLWDSH 78
DB 8 ALLLLPLLRSG-----TEGARTLRACGPKFKNRNVGGENALEGEPWQVSIQRNGH 61
QY 79 VCGVSLSHRWALTAACHFTYSDLSDPGSMVQFQOLTSMPFWSLQ-----AYTRYF 133
DB 62 FCGSLIAPTWLTAAHCF---SNTSDISIYQLLAL-----KLQPGPHALYVP-- 109
QY 134 VSNILSPRYLG-NSPYDIALVKLSAPVTKHIQICLOASTFEFENRTDQWTCGWYI 192
DB 110 VKQVKSNFQVQWASSADVALVELQGPVTFNVLVCLDPDPVIFESGMCNMTWGWSP 169
QY 193 KEDEALPSPTLQEVQVAINNMCNHLF---LKYSPR-KDIFGDMVCAGNAQGGKDACF 248
DB 170 SEQDRLENPRVLQKLAVIDTPKCNLLYNKDVESDFOLKTKDDMLCAGFAEGKDAC 229
QY 249 GDSGGPLACNKGWLWQIGVGVGCGRRNRPVTVNISHHPEWTKLMAQ 300
DB 230 GDSGGPLVCLVDQSWQAGVISWEGCARRNRPGVIRVTSHHKHWHQIPE 281

RESULT 8
Q80XZ3 PRELIMINARY; PRT; 311 AA.
AC Q80XZ3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Trypase gamma 1.
GN TP8G1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP Rattus norvegicus (Rat).
RA Li L., Wong G.W., Yang Y., Stevens R.L.;
RT "Identification of rat trypase gamma hydrophobic extension.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY196208; AAC00840.1; -.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR Pfam; PF00089; trypsin; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 311 AA; 32807 MW; 78362611679398FF CRC64;

Query Match 31.9%; Score 572.5; DB 11; Length 311;
Best Local Similarity 41.7%; Pred. No. 4.6e-45;
Matches 129; Conservative 39; Mismatches 112; Indels 29; Gaps 8;

QY 24 LLARAGLRKPSQEAAPLSGCGRRVITSRIYGGEDAEALGRWPQGSRLWDHVCVGS 83
DB 11 LLAVPGCQPVSHAG-----SRIVGHAQAQAGAPWQASLRILQKVHVCVGS 58
QY 84 LLSRWALTAACHFTYSDLSDPGSMVQFQOLTSMPFWSLQAYTRYFVSNILSPRY 143
DB 59 LLSFEVLTAAACHFSGVNSSD---YEVHLGLTI-----TLSPFSTVKQIIMVSSAPG 110
QY 144 LGNSPYDIALVKLSAPVTKHIQICLOASTFEFENRTDQWTCGWYIKDEALPSPT 203
DB 111 PFGSGDIALVQLATPVALSSQVQVCLPEASADPHGQMCQWTCGWYQSGEPLKPEYN 170

Query Match 31.9%; Score 571.5; DB 11; Length 331;
Best Local Similarity 42.8%; Pred. No. 6.2e-45;
Matches 127; Conservative 36; Mismatches 101; Indels 33; Gaps 7;

QY 42 LSGPCGRRVITSRIYGGEDAEALGRWPQGSRLWDHVCVGSLLSHRWALTAACHFTYS 101
DB 41 LDSVCGRRPRTSGRIVSQDAQLGRWPQVSVRENGAHVCGSLIADWLVLTAAHCFNQ 100
QY 102 DLSDPSCMWVQFQOLTSMPF---WSLQAYTRYFVSNILSPRYLG--NSPYDIALVK 156
DB 101 SLST---YTVLLGTISYPEDNEPKELRA-----VAQFKHPSYADSHSSGDIALV 151
QY 157 SAPVYTKHIQICLOASTFEFENRTDQWTCGWYIKDEALPSPTLQEVQVAINNMS 216
DB 152 ASPISFNDMVLPVCLPKPGDPLDPGTCMTWGTGHWGHIGTQPLPPPTLQELQVPLDAET 211
QY 217 CNHLFLKYSF---RKDIFGDMVCAGNAQGGKDACFGDSGGLACNKGWLWYQIGVSWGV 273
DB 212 CNTYOENSTPGTEPTEPVILEGMLCAGPQQGKKACNGDSGGLVCDINDWVIQAGVSWGS 271
QY 274 GCGRRNRPVTVNISHHFEWIKLMAQSGMSQDPSWPLL-----FPFLWALPLAG 325
DB 272 DCALFKRPVTVNIVSYISWIKNTY-----WNLPMRGSPSPSLSGTFLUG 317
```

```

RESULT 10
Q80X17 PRELIMINARY; PRT; 331 AA.
AC Q80X17;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Trypsase 5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=BAUB/c; TISSUE=Brain;
RA Wong G.W., Yasuda S., Stevens R.L., Li L.;
RT "Cloning and characterization of mouse trypsin-5 (mT5).";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY266139; AAP23216.1; -
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser. trypsin.
DR InterPro; IPR001254; Peptidase S1.
DR Pfam; PF00089; trypsin_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
SQ SEQUENCE 331 AA; 35640 MW; B1B366F32EF720377 CRC64;

Query Match 31.7%; Score 568.5; DB 11; Length 331;
Best Local Similarity 42.4%; Pred. No. 1.2e-44;
Matches 126; Conservative 37; Mismatches 101; Indels 33; Gaps 7;

QY 42 LSGCGRRVITSRVGGDEALGRWPMQSLRLWDSHVCSLLSHRWALTAHCFRTYS 101
DB ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
QY 102 DLSDFGMMVQGLTSMPSF---WSLOAYTRVFNIVYSPRYLG--NSPVDIALVKL 156
DB || : : : : : || : : : : : || : : : : : || : : : : : || : : : : :
QY 101 SLSI---YTVLLGVISSYPEDNEPKELRA-----VAQFIKHPYSADSHSGDIALVQL 151
DB || : : : : : || : : : : : || : : : : : || : : : : : || : : : : :
QY 157 SAPVTYTKHIQPICLQASTFEFENRTDCWVTGWSGVKEDEALPSPHTLQEVQVAIINNSM 216
DB || : : : : : || : : : : : || : : : : : || : : : : : || : : : : :
QY 152 ASPTSFNDYMLPVCLPKPGDPLDPTGTCWVTGWSGHGTNQPLPPFTLQELQPLDAET 211
DB || : : : : : || : : : : : || : : : : : || : : : : : || : : : : :
QY 217 CNHLFLKYSF---KXIDFGDMVCAGNAQGGKACFGSGGGLACNKNGLWYQIGWSWGV 273
DB || : : : : : || : : : : : || : : : : : || : : : : : || : : : : :
QY 212 CNTYYQENSIPGTEFVILEGLMCLAGFOEGKKDACNGDSGGPLVCDINDVWIQAGVWSGS 271
DB || : : : : : || : : : : : || : : : : : || : : : : : || : : : : :
QY 274 GCGRPNRPGVYTNISHPFEWIKLMAQSGMSQPPSPWLL-----PEPILLWALPLL 325
DB || : : : : : || : : : : : || : : : : : || : : : : : || : : : : :
QY 272 DCALFKRPGVYTNISVISIQNTW-----WNLEPMRGRGFSLSGTPLLG 317
DB || : : : : : || : : : : : || : : : : : || : : : : : || : : : : :

RESULT 11
Q99L44 PRELIMINARY; PRT; 339 AA.
AC Q99L44;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Similar to protease, serine, 8 (Prostasin).
GN PRS8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;

```

```

RN [1] SEQUENCE FROM N.A.
RP Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2] SEQUENCE FROM N.A.
RC STRAIN=129/SVJ, and Swiss; TISSUE=Lung;
RA Verghese G.M., Caughey G.H.;
RT "Molecular cloning and characterization of mouse prostasin, a type I
RT membrane-associated serine protease of the gamma-trypsin/prostasin
RT gene family.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [3] SEQUENCE FROM N.A.
RP Kitamura K., Takefumi N., Kimio T.;
RL "mouse serine protease.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; BC003851; AA03851.1; -
DR EMBL; AF378086; AAL06320.1; -
DR EMBL; AF378085; AAL06319.1; -
DR EMBL; AB038244; BAB82496.1; -
DR HSP; P00734; IUVS.
DR MGD; MGI:1923810; Prss8.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0004233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser. trypsin.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 339 AA; 36216 MW; BC2DE88BC057AF10 CRC64;

Query Match 31.6%; Score 565.5; DB 11; Length 339;
Best Local Similarity 38.2%; Pred. No. 2.3e-44;
Matches 133; Conservative 57; Mismatches 87; Indels 71; Gaps 13;

QY 20 LLLALLARAGLRKPEQEAAPLSPGCGRRVITSRVGGDEALGRWPMQSLRLWDSHV 79
DB ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
QY 17 ILLLLGLLQSGIR-ADGTEAS-----CG-AVIQPRITGGSAAKPGQWPMQVSIYDGNHV 69
DB || : : : : : || : : : : : || : : : : : || : : : : : || : : : : :
QY 80 CGVSLLSHRWALTAHCF-----ETSDLSDFSGMMVQFG--QLTSMPSFWSLOAYTR 131
DB || : : : : : || : : : : : || : : : : : || : : : : : || : : : : :
QY 70 CGSIVSNKNVWVSAACFPREHSREAYE-----VKLGAHQGLDS-----YSN 110
DB || : : : : : || : : : : : || : : : : : || : : : : : || : : : : :
QY 132 YFVSNIVLSRYLGNSPY-----DIALVKLSAPVTYTKHIQPICLQASTFEFENRTDC 184
DB || : : : : : || : : : : : || : : : : : || : : : : : || : : : : :
QY 111 DIV--VHTVAQIITHSSYREBSGQDIALIRLSPTVFESYRIRICLPAAKASFPNGLFC 168
DB || : : : : : || : : : : : || : : : : : || : : : : : || : : : : :
QY 185 WYTGNGYIKEDALPSPHTLQEVQVAIINNSMCHLFLKYSFRKD---IPDMVCAGNAQ 241
DB || : : : : : || : : : : : || : : : : : || : : : : : || : : : : :
QY 169 TVTGWGHVAPSVSLQTPRFLQQLLEVLTISRETCLYNINAVPEPHTIQDMLCAGYVK 228
DB || : : : : : || : : : : : || : : : : : || : : : : : || : : : : :
QY 242 GGDACFGDGGGLACNKNGLWYQIGVYSGVCGRPNRPGVYTNISHPFEWIK----- 295
DB || : : : : : || : : : : : || : : : : : || : : : : : || : : : : :
QY 229 GGDACQGDSDSGPLSCPNEGIWLAGIVSWGDACAFNRPGVYTLTSTYASWIIHHVAEL 288
DB || : : : : : || : : : : : || : : : : : || : : : : : || : : : : :
QY 296 --KLMAQSGMSQPD-----PSW-----PLLPFLWALPLL 324
DB || : : : : : || : : : : : || : : : : : || : : : : : || : : : : :
QY 289 QPRVVPQTESQPDGHLCHNHHPVFSSAAAPKLLRPVLFPLGLTLGLL 336
DB || : : : : : || : : : : : || : : : : : || : : : : : || : : : : :

RESULT 12
Q9DGR3 PRELIMINARY; PRT; 317 AA.
ID Q9DGR3
AC Q9DGR3;

```

DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Embryonic serine protease-1.
 GN XESP-1.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=20363741; PubMed=10903452;
 RA Yamada K., Takabatake T., Takehima K.;
 RT "Isolation and characterization of three novel serine protease genes
 from *Xenopus laevis*.";
 RL Gene 252:209-216(2000).
 DR EMBL; AB038496; BAB08216.1; --
 DR HSSP; P00763; 1DPO.
 DR MEROPS; S01.048; --
 DR GO; GO:004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008223; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR009003; Cys Ser trypsin.
 DR InterPro; IPR001254; Peptidase_S1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Protease; Serine protease.
 SQ SEQUENCE 317 AA; 34413 MW; EEC78A9F46D138FE CRC64;

 Query Match 31.3%; Score 561; DB 13; Length 317;
 Best Local Similarity 41.5%; Pred. NO. 5.6e-44;
 Matches 127; Conservative 34; Mismatches 105; Indels 40; Gaps 9;

 QY 39 AAPLSPGCGRRVITSRIVGGDAELGRWPQGSRLWDSHVGSLSHWALTAHCFE 98
 DB 28 APPL---CSSPFSSRIVGDTTRQGANPWQSLFENGSHICGSLISDQWLTHATHCIE 84
 QY 99 TVSDLSPPSGMWVQFQGLTSMPSFNSLQAYTRYFVSN-----IYLSPLYG-NS 147
 DB 85 -HPDL-PSGCGVRLG-----AV--QLYVKNPHEMTVKVDIIYINSEFNGPCT 127
 QY 148 PYDIALVKLSAPVYTKHIQICLOASTEFENRDTCDWTGNGYKEDEALPSPTLQEV 207
 DB 128 SGDIALLKUSSPKFTFEYILPICLPASPTVFSGTECTIGWQTGSEVPLQYPATLOKV 187
 QY 208 QVAIINNSMCHLFLKYSFRKD---IFGDMVCAGNAQGGKACFDGSGGLACNKGILW 263
 DB 188 MWPIINRDCERKMYHINSVISETEILLQSDICAGVQAGKQCGQDSGGLVCKIQGF 247
 QY 264 YQIGVSVWGCGGRPNRPGVYTNISHHFWIKLMAQS-----GMSQDDPSWPLFFPL 318
 DB 248 YQAGIVSWGERCAAKNRPGVYTFVPAYETWISERSVISFKPTSSSSSSSVLRASAIL 307
 QY 319 WALPPL 324
 DB 308 LGVSL 313

 RESULT 13
 Q8BJV6
 ID Q8BJV6 PRELIMINARY; PRT; 340 AA.
 AC Q8BJV6;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Prostasin.

GN PRS8.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RN SEQUENCE FROM N.A.
 RX STRAIN=C57BL/6J; TISSUE=Eye;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; AK078636; BAC37362.1; --
 DR MGD; MGI:1923810; Prs8.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR009003; Cys Ser trypsin.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 SQ SEQUENCE 340 AA; 36503 MW; 3C2540E9B3A81C8A CRC64;

 Query Match 30.7%; Score 550; DB 11; Length 340;
 Best Local Similarity 37.4%; Pred. No. 6.5e-43;
 Matches 131; Conservative 57; Mismatches 88; Indels 74; Gaps 14;

 QY 20 LLLALLARAGLRKPESQEAAPLSPGCGRRVITSRIVGGDAEL-GRWPQGSRLWDSH 78
 DB 17 ILDLLGLQSGIR-ADGTEAS-----CG-AVIQRTGGQGWSPGQWVQVITYDGNH 69
 QY 79 VCGVSLSHWALTAHCF-----ETYSDLSPSGMWVQFQGLTSMPSFNSLQAYTRY 132
 DB 70 VCGSVSVNKNVWSAHCFFREHREAYE-----VKLGD-----HQLDSY---- 109
 QY 133 FVSN---IYLSPLYGNSPY-----DIALVKLSAPVYTKHIQICLOASTFEFENRT 182
 DB 110 --SNDTVHTVAQIITHSSYREESQGDIALIRLSPVTFEYIRPICLPANASFENGL 167
 QY 183 DCWTGNGYKEDEALPSPTLQEVQVAIINNSMCHLFLKYSFRKD---IFGDMVCAGN 239
 DB 168 HCTVTHGHWAPSVLSQTPRLOQLEVPLISRTCSCLYNINAVPEPHTIQDMLCAGY 227
 QY 240 AQGKDACFDGSGGLACNKGILWYQIGVSVWGCGGRPNRPGVYTNISHHFWIQ---- 295
 DB 228 VKGKDACQGDGSGPLSCPMEGIWYLAGIVSGDACGAPNRPVYTLTSTYASWTHHVA 287
 QY 296 ----KLMAQSGMSQPD-----PSW-----PLFPFLWALPPL 324
 DB 288 ELQPRVVPQTQESQPDGHLNHHVFPSSAAAPKLLRPVLPFLPLGLTLGLL 337

 RESULT 14
 Q7TML0
 ID Q7TML0 PRELIMINARY; PRT; 307 AA.
 AC Q7TML0;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE RIKEN cDNA 473401N09.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RN SEQUENCE FROM N.A.

```
RC STRAIN=C57BL/6J; TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Narusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.B., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Joquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalski U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences".
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC055854; AAH55854.1; --
SQ SEQUENCE 307 AA; 33431 MW; 58692F29355B704E CRC64;

Query Match 29.8%; Score 534.5; DB 11; Length 307;
Best Local Similarity 38.4%; Pred. No. 1.6e-41;
Matches 114; Conservative 53; Mismatches 103; Indels 27; Gaps 6;

QY 20 LLLALLARAGLRKPESQEAAPLSPGCGRRVITSRIVGGEDAEGLRWPMQGLRLWDSHV 79
DB 19 ILLVLLTSTA-----PISAAITRVSPDCGKPOQLNRIVGGEDSDMDAQWPIVSLKXSHR 74
QY 80 CGVSLLSHRWALTAACFETYSDDLSPSGMWVQFGLTSMPSFWSLQAYTR---YFVSN 136
DB 75 CAGSLTLNRVVTAAACFK--SNMDKPSLPVLLGA-----WKLGPSPRSQKVGIAW 125
QY 137 IYLSPRY--LGNSPYDIALVKLSAPVTYTKHIQICLQASTFEFENRTDCWWTGVIKE 194
DB 126 VLPHRYGWSKGTADIALVLEHSIQFSEILPCLPDSVRUPPKTDICWAGWSIQD 185
QY 135 DEALPSPTLQEQVVAIINNSCNHLFLKYFRKDIIFGDMVCAGNAQGGKDACFGDSGGP 254
DB 186 GVPLPHTQTLQKLVPIIDSELCKSLYWRGAGQEAITEGMLCAGYLEGERDACLDGGP 245
QY 255 LACNKGWLYQIGVUSWVGCGRPNRPQVYTNISHHFEWIKL-----MAQSG 302
DB 246 LMCQVDHLLTGLTIISWGEGCAERNRPGVYTSLLAHRVQVIRIVQGVQLADSG 302

RESULT 15
O88781 PRELIMINARY; PRT; 297 AA.
AC O88781;
DT 01-NOV-1998 (TremBLrel. 08, Created)
DT 01-NOV-1998 (TremBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Serine protease precursor (Fragment).
GN BSP2.
OS Rattus rattus (Black rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Fisher; TISSUE=Brain;
RX MEDLINE=98389725; PubMed=9722524;
RA Davies B.J., Fickard B.S., Steel M., Morris R.G., Lathe R.;
```

```
RT "Serine Proteases in Rodent Hippocampus.";
RL J. Biol. Chem. 273:23004-23011 (1998).
DR EMBL; AJ005642; CAA06644.1; --
DR HSP; P00763; IDPO.
DR MEROPS; S01.252; --
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Hydrolase; Protease; Serine protease; Signal.
KW NON_TER 1 1
FT SIGNAL <1 23 POTENTIAL.
FT CHAIN 24 297 SERINE_PROTEASE.
SQ SEQUENCE 297 AA; 32086 MW; 6DA25C6633D6AB55 CRC64;

Query Match 29.8%; Score 533.5; DB 11; Length 297;
Best Local Similarity 37.5%; Pred. No. 1.9e-41;
Matches 115; Conservative 55; Mismatches 102; Indels 35; Gaps 8;

QY 16 ARGA----LLALLARAGLRKPESQEAAPLSPG--PCGRRVITSRIVGGEDAEGLRWPMQ 69
DB 1 ARGSSPPGLTLFILLPSA-----TVSAANIRGSPDCGKPOQLNRVGGEDSADAQWPI 54
QY 70 GSLRLWDHVGCVSLLSHRWALTAACFETYSDDLSPSGMWVQFGLTSMPSFWSL---Q 126
DB 55 VSILKNGSHHCAGSLTLNRVWVSAACFS--SNMDKPSFPYVLLGA-----WKLGNPG 105
QY 127 AYTRYFVSNIYLSPRY--LGNSPYDIALVKLSAPVTYTKHIQICLQASTFEFENRTDC 184
DB 106 PRSQVGIASVLPHPRYSRKGTADIALVLERIQFSEILPCLPDSVSLPNTINC 165
QY 185 WYTGWGYIKEDBALPSPTLQEQVVAIINNSCNHLFLKYFRKDIIFGDMVCAGNAQGGK 244
DB 166 WIAGWSIQDGVLPRLPQTLQKLVPIIDSELCKSLYWRGAGQEAITEGMLCAGYLEGR 225
QY 245 DACFGDSGGPLACNKGWLYQIGVUSWVGCGRPNRPQVYTNISHHFEWIKL----- 297
DB 226 DACLDGSGGLMCMQVDHLLTGLTIISWGEGCAERNRPGVYTSLLAHRVQVIRIVQGVQLR 285
QY 298 --MAQSG 302
DB 286 GRLADSG 292

Search completed: April 6, 2004, 14:13:05
Job time : 47 secs
```


; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,598
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 257
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-909-320-257

Query Match 96.4%; Score 1728; DB 9; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.8e-161; Indels 0; Gaps 0;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 MGARGALLALLARAGLRKPESQEAAPLSGCGRRVITSRIVGGEDAEALGRWPQGSRLR 73
DB 1 MGARGALLALLARAGLRKPESQEAAPLSGCGRRVITSRIVGGEDAEALGRWPQGSRLR 60
QY 74 LWDHVCVGSLLSHRWALTAACHCFETYSDDLSDPSGMMVQFQGLTSMPSFWSLQAYTRYF 133
DB 61 LWDHVCVGSLLSHRWALTAACHCFETYSDDLSDPSGMMVQFQGLTSMPSFWSLQAYTRYF 120
QY 134 VSNLYLSPRYLGNPSYDIALVKLSAPVITYTKHIQPICLQASTFEFFENRTDCWVTGWGYIK 193
DB 121 VSNLYLSPRYLGNPSYDIALVKLSAPVITYTKHIQPICLQASTFEFFENRTDCWVTGWGYIK 180
QY 194 EDEALPSHTLQEVQVVAIINNSMCNHLFLKYSFRKIDFGDMVCAGNAQGGKACFGDSGG 253
DB 181 EDEALPSHTLQEVQVVAIINNSMCNHLFLKYSFRKIDFGDMVCAGNAQGGKACFGDSGG 240
QY 254 PLACNKGMLWQIGVVSVMGCGGRNRPVGTNTSHHFEWIKLMAQSGMSQPDPSWPLL 313
DB 241 PLACNKGMLWQIGVVSVMGCGGRNRPVGTNTSHHFEWIKLMAQSGMSQPDPSWPLL 300
QY 314 FFPLLWALPLGPV 327
DB 301 FFPLLWALPLGPV 314

RESULT 2
US-09-885-441-14
; Sequence 14, Application US/09885441
; Patent No. US20020146407A1
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong

; TITLE OF INVENTION: Regulation of Human Eosinophil Serine
; FILE OF INVENTION: Protease-1-Like Enzyme
; FILE REFERENCE: 04974.00512
; CURRENT APPLICATION NUMBER: US/09/885,441
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/212,844
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: US 60/244,171
; PRIOR FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: US 60/279,766
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: PCT/
; PRIOR FILING DATE: 2001-06-20
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-885-441-14

Query Match 96.4%; Score 1728; DB 9; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.8e-161; Indels 0; Gaps 0;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 MGARGALLALLARAGLRKPESQEAAPLSGCGRRVITSRIVGGEDAEALGRWPQGSRLR 73
DB 1 MGARGALLALLARAGLRKPESQEAAPLSGCGRRVITSRIVGGEDAEALGRWPQGSRLR 60
QY 74 LWDHVCVGSLLSHRWALTAACHCFETYSDDLSDPSGMMVQFQGLTSMPSFWSLQAYTRYF 133
DB 61 LWDHVCVGSLLSHRWALTAACHCFETYSDDLSDPSGMMVQFQGLTSMPSFWSLQAYTRYF 120
QY 134 VSNLYLSPRYLGNPSYDIALVKLSAPVITYTKHIQPICLQASTFEFFENRTDCWVTGWGYIK 193
DB 121 VSNLYLSPRYLGNPSYDIALVKLSAPVITYTKHIQPICLQASTFEFFENRTDCWVTGWGYIK 180
QY 194 EDEALPSHTLQEVQVVAIINNSMCNHLFLKYSFRKIDFGDMVCAGNAQGGKACFGDSGG 253
DB 181 EDEALPSHTLQEVQVVAIINNSMCNHLFLKYSFRKIDFGDMVCAGNAQGGKACFGDSGG 240
QY 254 PLACNKGMLWQIGVVSVMGCGGRNRPVGTNTSHHFEWIKLMAQSGMSQPDPSWPLL 313
DB 241 PLACNKGMLWQIGVVSVMGCGGRNRPVGTNTSHHFEWIKLMAQSGMSQPDPSWPLL 300
QY 314 FFPLLWALPLGPV 327
DB 301 FFPLLWALPLGPV 314

RESULT 3
US-09-909-088B-257
; Sequence 257, Application US/09909088B
; Patent No. US20020146709A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mather, Jennie P.

APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909,088B
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 257
LENGTH: 314
TYPE: PRT
ORGANISM: Homo Sapien
US-09-909-088B-257

Query Match 96.4%; Score 1728; DB 9; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.8e-161;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 MGARGALLALLARAGLRKPESQEAAPLSGPGRRVITSRIVGGEDAEALGRWPQGSRLR 73
DB 1 MGARGALLALLARAGLRKPESQEAAPLSGPGRRVITSRIVGGEDAEALGRWPQGSRLR 60
QY 74 LWDSHVCGVSLLSHRWALTAHCFETYSDLSDSGGMWQFQGLTSPSPFWSLQAYTRYF 133
DB 61 LWDSHVCGVSLLSHRWALTAHCFETYSDLSDSGGMWQFQGLTSPSPFWSLQAYTRYF 120
QY 134 VSNILSPRYLGNSPDYIALVKLSAPVYTKHQIPICLQASTFEFENRDCWVTGWGVIK 193
DB 121 VSNILSPRYLGNSPDYIALVKLSAPVYTKHQIPICLQASTFEFENRDCWVTGWGVIK 180
QY 194 EDEALPSPTLQEQVAIVAINNSCNHLFLKYSFRKDFGDMVCAGNAQGGKACFGDSGG 253
DB 181 EDEALPSPTLQEQVAIVAINNSCNHLFLKYSFRKDFGDMVCAGNAQGGKACFGDSGG 240

QY 254 PLACNKNGLWYQIGVYSGVGCGRPNRPGVYTNISHHFEWIKLMAQSGMSQDDPSWPLL 313
DB 241 PLACNKNGLWYQIGVYSGVGCGRPNRPGVYTNISHHFEWIKLMAQSGMSQDDPSWPLL 300
QY 314 FFPLLWALPULGPV 327
DB 301 FFPLLWALPULGPV 314

RESULT 4
US-09-905-291A-257
Sequence 257, Application US/09905291A
Patent No. US20020160374A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Flivaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,291A
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911

```
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 257
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-905-291A-257

Query Match          96.4%; Score 1728; DB 9; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.8e-161;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 MGARGALLALLARAGLRKPESQEAAPLSGCGRRVITSRIVGGDAELGRWPWGSLR 73
DB 1 MGARGALLALLARAGLRKPESQEAAPLSGCGRRVITSRIVGGDAELGRWPWGSLR 60
QY 74 LWDHSHVCGVSLLSHRWALTAACHCFETYSDDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYF 133
DB 61 LWDHSHVCGVSLLSHRWALTAACHCFETYSDDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYF 120
QY 134 VSNIIYLSPRYLGNSPYDIALVKLSAPVYTKHIQICLQASTFEFENRTDCWVTGWGVIK 193
DB 121 VSNIIYLSPRYLGNSPYDIALVKLSAPVYTKHIQICLQASTFEFENRTDCWVTGWGVIK 180
QY 194 EDEALPSHTLQEQVQVAIIINNSMCNHLFLKYSFRKIDFGDMVCAGNAQGGKDACFGDSGG 253
DB 181 EDEALPSHTLQEQVQVAIIINNSMCNHLFLKYSFRKIDFGDMVCAGNAQGGKDACFGDSGG 240
QY 254 PLACNKNGLWYQIGVSWGCGRRNRPVYTNISHHFEWIKLMAQSGMSQDPDPSWPLL 313
DB 241 PLACNKNGLWYQIGVSWGCGRRNRPVYTNISHHFEWIKLMAQSGMSQDPDPSWPLL 300
QY 314 FFPLLWALPLLGVPV 327
DB 301 FFPLLWALPLLGVPV 314

RESULT 5
US-09-902-853-257
; Sequence 257, Application US/09902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
```

```
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,853
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US/09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 257
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-902-853-257

Query Match          96.4%; Score 1728; DB 9; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.8e-161;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 MGARGALLALLARAGLRKPESQEAAPLSGCGRRVITSRIVGGDAELGRWPWGSLR 73
DB 1 MGARGALLALLARAGLRKPESQEAAPLSGCGRRVITSRIVGGDAELGRWPWGSLR 60
QY 74 LWDHSHVCGVSLLSHRWALTAACHCFETYSDDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYF 133
DB 61 LWDHSHVCGVSLLSHRWALTAACHCFETYSDDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYF 120
QY 134 VSNIIYLSPRYLGNSPYDIALVKLSAPVYTKHIQICLQASTFEFENRTDCWVTGWGVIK 193
DB 121 VSNIIYLSPRYLGNSPYDIALVKLSAPVYTKHIQICLQASTFEFENRTDCWVTGWGVIK 180
QY 194 EDEALPSHTLQEQVQVAIIINNSMCNHLFLKYSFRKIDFGDMVCAGNAQGGKDACFGDSGG 253
DB 181 EDEALPSHTLQEQVQVAIIINNSMCNHLFLKYSFRKIDFGDMVCAGNAQGGKDACFGDSGG 240
QY 254 PLACNKNGLWYQIGVSWGCGRRNRPVYTNISHHFEWIKLMAQSGMSQDPDPSWPLL 313
DB 241 PLACNKNGLWYQIGVSWGCGRRNRPVYTNISHHFEWIKLMAQSGMSQDPDPSWPLL 300
QY 314 FFPLLWALPLLGVPV 327
DB 301 FFPLLWALPLLGVPV 314
```

RESULT 6
US-09-907-824-257
; Sequence 257, Application US/09907824
; Publication No. US20020197671A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,824
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 257

LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-824-257
Query Match 96.4%; Score 1728; DB 9; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.8e-161; Indels 0; Gaps 0;
Matches 314; Conservative 0; Mismatches 0;
QY 14 MGARGALLALLARAGLRKPESQEAAPLSPGQRRVITSRIVGGBDAELGRWPWQSLR 73
Db 1 MGARGALLALLARAGLRKPESQEAAPLSPGQRRVITSRIVGGBDAELGRWPWQSLR 60
QY 74 LWDSHVGVSLLSHRWALTAHCFETYSDDLSPSGMWVQFGOLTSMPFSFSLQAYTYRF 133
Db 61 LWDSHVGVSLLSHRWALTAHCFETYSDDLSPSGMWVQFGOLTSMPFSFSLQAYTYRF 120
QY 134 VSNIVLSPRYLGNPSYDIALVKLSAPVTYTKHIQICLOASTFFENRTDCWVTGWYIK 193
Db 121 VSNIVLSPRYLGNPSYDIALVKLSAPVTYTKHIQICLOASTFFENRTDCWVTGWYIK 180
QY 194 EDEALPSPHTLQEVQVVAIIINNSMCNHLFLKYSFKDIFGDMVCAGNAGGKDACFGDSGG 253
Db 181 EDEALPSPHTLQEVQVVAIIINNSMCNHLFLKYSFKDIFGDMVCAGNAGGKDACFGDSGG 240
QY 254 PLACNKNGLWYQIGVSWGVGCGRPNRPVYVYTNISHHFEMWIKLMAQSGMSQDPSPWPLL 313
Db 241 PLACNKNGLWYQIGVSWGVGCGRPNRPVYVYTNISHHFEMWIKLMAQSGMSQDPSPWPLL 300
QY 314 FPPLLMALPLLPV 327
Db 301 FPPLLMALPLLPV 314

RESULT 7

US-09-907-841-257
; Sequence 257, Application US/09907841
; Publication No. US20020198366A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,841
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07

;; PRIOR APPLICATION NUMBER: US 60/145,698
;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: US 60/146,222
;; PRIOR FILING DATE: 1999-07-28
;; PRIOR APPLICATION NUMBER: PCT/US99/20594
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/20944
;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/21547
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/23089
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: PCT/US99/28214
;; PRIOR FILING DATE: 1999-11-29
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 257
;; LENGTH: 314
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-907-841-257

Query Match 96.4%; Score 1728; DB 9; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.8e-161; Indels 0; Gaps 0;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 MGARGALLALLARAGLRKPESQEAAPLSGCGRRVITSRIVGGDAELGRWPWGSLR 73
DB 1 MGARGALLALLARAGLRKPESQEAAPLSGCGRRVITSRIVGGDAELGRWPWGSLR 60

QY 74 LWDSHVCGVSLLSHRWALTAACHFETYSDDLSPSGMWVQFGQLTSMPSLQAYYTRYF 133
DB 61 LWDSHVCGVSLLSHRWALTAACHFETYSDDLSPSGMWVQFGQLTSMPSLQAYYTRYF 120

QY 134 VSNIIYLSPRYLGNSPYDIALVKLSAPVTTYTKHIQICLQASTFFENRTDCWVTGWGIK 193
DB 121 VSNIIYLSPRYLGNSPYDIALVKLSAPVTTYTKHIQICLQASTFFENRTDCWVTGWGIK 180

QY 194 EDEALPSHTLQEOVQVAIINSMCNHLEFKYSFKDIFGDMVCAGNAGGKACFGDSGG 253
DB 181 EDEALPSHTLQEOVQVAIINSMCNHLEFKYSFKDIFGDMVCAGNAGGKACFGDSGG 240

QY 254 PLACNKGILWYQIGVVSWGVGCGRENRPVGTYNISHHFEWIKLMAQSGMSQPPDSNPLL 313
DB 241 PLACNKGILWYQIGVVSWGVGCGRENRPVGTYNISHHFEWIKLMAQSGMSQPPDSNPLL 300

QY 314 FPFLWALPLGPV 327
DB 301 FPFLWALPLGPV 314

RESULT 8

US-09-904-011-257
;; Sequence 257, Application US/09904011
;; Publication NO. US20030003530A1
;; GENERAL INFORMATION:
;; APPLICANT: Genentech, Inc.
;; APPLICANT: Ashkenazi, Avi
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, A.
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, Christopher J.
;; APPLICANT: Gurney, Austin L.

Query Match 96.4%; Score 1728; DB 10; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.8e-161; Indels 0; Gaps 0;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 MGARGALLALLARAGLRKPESQEAAPLSGCGRRVITSRIVGGDAELGRWPWGSLR 73
DB 1 MGARGALLALLARAGLRKPESQEAAPLSGCGRRVITSRIVGGDAELGRWPWGSLR 60

QY 74 LWDSHVCGVSLLSHRWALTAACHFETYSDDLSPSGMWVQFGQLTSMPSLQAYYTRYF 133
DB 61 LWDSHVCGVSLLSHRWALTAACHFETYSDDLSPSGMWVQFGQLTSMPSLQAYYTRYF 120

QY 134 VSNIIYLSPRYLGNSPYDIALVKLSAPVTTYTKHIQICLQASTFFENRTDCWVTGWGIK 193
DB 121 VSNIIYLSPRYLGNSPYDIALVKLSAPVTTYTKHIQICLQASTFFENRTDCWVTGWGIK 180

QY 194 EDEALPSHTLOEVQVAIINNSMCNHLKYSFRKDIIFGDMVCAGNAQGGKDACFGDSGG 253
D6 181 EDEALPSHTLOEVQVAIINNSMCNHLKYSFRKDIIFGDMVCAGNAQGGKDACFGDSGG 240
QY 254 PLACNKGMLWQIGVSVGCGRPNRPVYTNISHHFEWIKLMAQSGMSQDPDPSPWLL 313
D6 241 PLACNKGMLWQIGVSVGCGRPNRPVYTNISHHFEWIKLMAQSGMSQDPDPSPWLL 300
QY 314 FFLWALPLIGPV 327
D6 301 FFLWALPLIGPV 314

RESULT 9
US-09-906-742-257
; Sequence 257, Application US/09906742
; Publication No. US20030023054A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,742
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-03
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30

; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 257
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-906-742-257

Query Match 96.4%; Score 1728; DB 10; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.8e-161;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 MGARGALLALLARAGLRKPEQEAAPLSGPGCRRVITSRIVGGDAELGRWPWQSLR 73
D6 1 MGARGALLALLARAGLRKPEQEAAPLSGPGCRRVITSRIVGGDAELGRWPWQSLR 60
QY 74 LWDHVGCVSLLSHRWALTAHCFETYSDLSDFSGMWVQFQLTSMPSWLSQAYTRYF 133
D6 61 LWDHVGCVSLLSHRWALTAHCFETYSDLSDFSGMWVQFQLTSMPSWLSQAYTRYF 120
QY 134 VSNITLSPRYLGNSPYDIALVKLSAPVYTKHIQICLOASTFEFENRTDCWVTGWYIK 193
D6 121 VSNITLSPRYLGNSPYDIALVKLSAPVYTKHIQICLOASTFEFENRTDCWVTGWYIK 180
QY 194 EDEALPSHTLOEVQVAIINNSMCNHLFLKYSFRKDIIFGDMVCAGNAQGGKDACFGDSGG 253
D6 181 EDEALPSHTLOEVQVAIINNSMCNHLFLKYSFRKDIIFGDMVCAGNAQGGKDACFGDSGG 240
QY 254 PLACNKGMLWQIGVSVGCGRPNRPVYTNISHHFEWIKLMAQSGMSQDPDPSPWLL 313
D6 241 PLACNKGMLWQIGVSVGCGRPNRPVYTNISHHFEWIKLMAQSGMSQDPDPSPWLL 300
QY 314 FFLWALPLIGPV 327
D6 301 FFLWALPLIGPV 314

RESULT 10
US-09-906-838-257
; Sequence 257, Application US/09906838
; Publication No. US20030027143A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,838
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 257
LENGTH: 314
TYPE: PRT
ORGANISM: Homo Sapien
US-09-906-838-257

Query Match 96.4%; Score 1728; DB 10; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.8e-161;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 MGARGALLALLARAGLAKPESQBAAPLSGCGRRVTSRIVGGEDAELOGRWPQGSRLR 73
DB 1 MGARGALLALLARAGLAKPESQBAAPLSGCGRRVTSRIVGGEDAELOGRWPQGSRLR 60

QY 74 LWDHVCVGLLSHRWALTAACFCFTYSDLPSCGMVQFGQLTSMPSFWSLQAYTYRF 133
DB 61 LWDHVCVGLLSHRWALTAACFCFTYSDLPSCGMVQFGQLTSMPSFWSLQAYTYRF 120

QY 134 VSNVILSPRYLGNSPYDIALVKLSAPVVTYTKHQICLQASTFPEFNTDCWVTGWGVIK 193
DB 121 VSNVILSPRYLGNSPYDIALVKLSAPVVTYTKHQICLQASTFPEFNTDCWVTGWGVIK 180

QY 194 EDEALPSPTLQEVQVAIINNSCNHLFLKYSFRKDIQDMVCAGNAOGGKDACFGDSGG 253
DB 181 EDEALPSPTLQEVQVAIINNSCNHLFLKYSFRKDIQDMVCAGNAOGGKDACFGDSGG 240

QY 254 PLACNKGGLWYQIGVSWGVCGRPNRPGVYTNISHHFWIKLMAQSGMSQDPSPWPLL 313
DB 241 PLACNKGGLWYQIGVSWGVCGRPNRPGVYTNISHHFWIKLMAQSGMSQDPSPWPLL 300

QY 314 FFPLLMALPLILGPV 327
DB 301 FFPLLMALPLILGPV 314

RESULT 11
US-09-907-613-257
Sequence 257, Application US/09907613
Publication No. US20030027145A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,613
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911


```

; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,942
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 257
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-613-257

Query Match          96.4%; Score 1728; DB 10; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.8e-161;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 MGARGALLALLARAGLRKPESQEAAPLSGPGGRRVITSRIVGGDEAELGRWPQGSRLR 73
DB 1 MGARGALLALLARAGLRKPESQEAAPLSGPGGRRVITSRIVGGDEAELGRWPQGSRLR 60
QY 74 LWDSHVCVGSLLSHRWALTAHCFETYSDSLSDPSGMMVQFQGLTSMPSFWSLQAYTRYF 133
DB 61 LWDSHVCVGSLLSHRWALTAHCFETYSDSLSDPSGMMVQFQGLTSMPSFWSLQAYTRYF 120
QY 134 VSNYILSPRYLGNSPYDIALVKLSAPVYTKHIQPICLQASTFEFENRTDCWVTGWGIK 193
DB 121 VSNYILSPRYLGNSPYDIALVKLSAPVYTKHIQPICLQASTFEFENRTDCWVTGWGIK 180
QY 194 EDEALPSPHTLQEVQVVAIINNMCNHLFLKYSFRKDFGDMVCAGNAGGKDACFGDSGG 253
DB 181 EDEALPSPHTLQEVQVVAIINNMCNHLFLKYSFRKDFGDMVCAGNAGGKDACFGDSGG 240
QY 254 PLACNKNGLWYQIGVSVGWGCGRRNRPVYTNISHHFEWIKLMAQSGMSQDPDSWPLL 313
DB 241 PLACNKNGLWYQIGVSVGWGCGRRNRPVYTNISHHFEWIKLMAQSGMSQDPDSWPLL 300
QY 314 FFPLLWALPLLGPV 327
DB 301 FFPLLWALPLLGPV 314

RESULT 12
US-09-907-942-257
; Sequence 257, Application US/09907942
; Publication No. US20030027146A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
```

```

Query Match          96.4%; Score 1728; DB 10; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.8e-161;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 MGARGALLALLARAGLRKPESQEAAPLSGPGGRRVITSRIVGGDEAELGRWPQGSRLR 73
DB 1 MGARGALLALLARAGLRKPESQEAAPLSGPGGRRVITSRIVGGDEAELGRWPQGSRLR 60
QY 74 LWDSHVCVGSLLSHRWALTAHCFETYSDSLSDPSGMMVQFQGLTSMPSFWSLQAYTRYF 133
DB 61 LWDSHVCVGSLLSHRWALTAHCFETYSDSLSDPSGMMVQFQGLTSMPSFWSLQAYTRYF 120
QY 134 VSNYILSPRYLGNSPYDIALVKLSAPVYTKHIQPICLQASTFEFENRTDCWVTGWGIK 193
DB 121 VSNYILSPRYLGNSPYDIALVKLSAPVYTKHIQPICLQASTFEFENRTDCWVTGWGIK 180
QY 194 EDEALPSPHTLQEVQVVAIINNMCNHLFLKYSFRKDFGDMVCAGNAGGKDACFGDSGG 253
DB 181 EDEALPSPHTLQEVQVVAIINNMCNHLFLKYSFRKDFGDMVCAGNAGGKDACFGDSGG 240
QY 254 PLACNKNGLWYQIGVSVGWGCGRRNRPVYTNISHHFEWIKLMAQSGMSQDPDSWPLL 313
DB 241 PLACNKNGLWYQIGVSVGWGCGRRNRPVYTNISHHFEWIKLMAQSGMSQDPDSWPLL 300
QY 314 FFPLLWALPLLGPV 327
DB 301 FFPLLWALPLLGPV 314

US-09-907-942-257
; TYPE: PRT
; ORGANISM: Homo Sapien
```

```
RESULT 13
US-09-904-859-257
; Sequence 257, Application US/09904859
; Publication No US20030036060A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pao, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,859
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 257

Query Match 96.4%; Score 1728; DB 10; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.8e-161; Indels 0; Gaps 0;
Matches 314; Conservative 0; Mismatches 0;
QY 14 MGARGALLALLARAGLRKPESQEAAPLSGPCRRVITSRIVGGEAEALGRWPQGSRLR 73
Db 1 MGARGALLALLARAGLRKPESQEAAPLSGPCRRVITSRIVGGEAEALGRWPQGSRLR 60
QY 74 LWDHSVGVSLSHRWALTAACFETYSDSLSDPSGMVQFQGLTSMSEFSLQAYTYRYF 133
Db 61 LWDHSVGVSLSHRWALTAACFETYSDSLSDPSGMVQFQGLTSMSEFSLQAYTYRYF 120
QY 134 VSNIVLSRYLGNSPYDIALVKLSAPVYTYTKHIQIPICLQASTFFEFNRDCWVTGWYIK 193
Db 121 VSNIVLSRYLGNSPYDIALVKLSAPVYTYTKHIQIPICLQASTFFEFNRDCWVTGWYIK 180
QY 194 IDEALPSHTLOEVQVVAIIINNSMCNHLFLKYSFRKIDFGDMVCAGNAGGKACFGDSGG 253
Db 181 IDEALPSHTLOEVQVVAIIINNSMCNHLFLKYSFRKIDFGDMVCAGNAGGKACFGDSGG 240
QY 254 PLACNKNGLWYQIGVWSGVGCGRPNRPGVVTNISHHFEWIKLMAQSGMSQPDPSWPLL 313
Db 241 PLACNKNGLWYQIGVWSGVGCGRPNRPGVVTNISHHFEWIKLMAQSGMSQPDPSWPLL 300
QY 314 FPFLWALPLLGPV 327
Db 301 FPFLWALPLLGPV 314

RESULT 14
US-09-909-204-257
; Sequence 257, Application US/09909204
; Publication No. US20030036061A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pao, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,204
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
```

APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: KJavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,820
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 257
LENGTH: 314
TYPE: PRT
ORGANISM: Homo Sapien
US-09-909-204-257

Query Match 96.4%; Score 1728; DB 10; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.8e-161;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 MGARGALLALLARAGLRKPSQEAAPLSGPGRRVITSRIVGGEADALGRWPGQSLR 73
DB 1 MGARGALLALLARAGLRKPSQEAAPLSGPGRRVITSRIVGGEADALGRWPGQSLR 60
QY 74 LWDSHVCGVSLLSHRWALTAACFCFETYSDDLSPSGMWVQFGLTSPFWSLQAYTYRYF 133
DB 61 LWDSHVCGVSLLSHRWALTAACFCFETYSDDLSPSGMWVQFGLTSPFWSLQAYTYRYF 120
QY 134 VSNYILSPRYLGNPSYDIALVKLSAPVYTKHIQPICLQASTFEPENRTDCWVTGNGYIK 193
DB 121 VSNYILSPRYLGNPSYDIALVKLSAPVYTKHIQPICLQASTFEPENRTDCWVTGNGYIK 180
QY 194 EDALSPHTLQVQVAIINNSMCHLFLKYSPKXDFGDMVCAGNAQGGKACFGDSGG 253
DB 181 EDALSPHTLQVQVAIINNSMCHLFLKYSPKXDFGDMVCAGNAQGGKACFGDSGG 240
QY 254 PLACNKNGLWYQIGVWSWGVCCGRPNRPVYTNISHHFWIQLKMAQSGMSQPDSPWPLL 313
DB 241 PLACNKNGLWYQIGVWSWGVCCGRPNRPVYTNISHHFWIQLKMAQSGMSQPDSPWPLL 300
QY 314 FPELLWALPLGPV 327
DB 301 FPELLWALPLGPV 314

RESULT 15
US-09-904-820-257
Sequence 257, Application US/09904820
Publication No. US20030036094A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi

Query Match 96.4%; Score 1728; DB 10; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.8e-161;
US-09-904-820-257

Matches	314;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	
Qy	14	MGARGALLALLARAGLRKPE	SOEAA	PLSGPCGRRVIT	SRI	VGGEDAE	ILGRWPMQ	GS	LR 73	
Db	1	MGARGALLALLARAGLRKPE	SOEAA	PLSGPCGRRVIT	SRI	VGGEDAE	ILGRWPMQ	GS	LR 60	
Qy	74	LWDSHVCVSLLSHRWALTA	AHCFETY	SDLSDFSGMWQ	FGQ	LTSMP	SPSWLSQ	AYTRYF	133	
Db	61	LWDSHVCVSLLSHRWALTA	AHCFETY	SDLSDFSGMWQ	FGQ	LTSMP	SPSWLSQ	AYTRYF	120	
Qy	134	VSNITLSPRVLGNSPYDIAL	VKL	SAPVYTKH	IQP	ICLOAST	FEFENR	TD	CWVTGWGYIK 193	
Db	121	VSNITLSPRVLGNSPYDIAL	VKL	SAPVYTKH	IQP	ICLOAST	FEFENR	TD	CWVTGWGYIK 180	
Qy	194	EDEALPSHTLQEVQVA	II	NNSMCNH	FLKYS	FRKDI	FGDMV	CAGNAQ	GGKDACPD	SG 253
Db	181	EDEALPSHTLQEVQVA	II	NNSMCNH	FLKYS	FRKDI	FGDMV	CAGNAQ	GGKDACPD	SG 240
Qy	254	PLACNKNGLWYQIGV	SWGVGCG	FRNRP	PGVY	TNISH	FEWIK	IQKMAQ	SGMSQ	PDPSWPLL 313
Db	241	PLACNKNGLWYQIGV	SWGVGCG	FRNRP	PGVY	TNISH	FEWIK	IQKMAQ	SGMSQ	PDPSWPLL 300
Qy	314	FFPLLWALPLIGPV	327							
Db	301	FFPLLWALPLIGPV	314							

Search completed: April 6, 2004, 14:18:55
Job time : 47 secs